```
June 27, 2002, 16:03:31; Search time 73.16 Seconds (without alignments) 215.589 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2: SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
3: SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
4: SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1992.DAT:*
5: SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:*
6: SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1994.DAT:*
7: SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1996.DAT:*
8: SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1996.DAT:*
9: SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1997.DAT:*
10: SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
11: SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
12: SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
13: SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
14: SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:*
15: SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*/SIDSI/gcgdata/hold-geneseq-geneseqp-embl/AA1981.DAT:*/SIDSI/gcgdata/hold-geneseqg-embl/AA1982.DAT:*/SIDSI/gcgdata/hold-geneseqg-embl/AA1983.DAT:*/SIDSI/gcgdata/hold-geneseqg-embl/AA1984.DAT:*/SIDSI/gcgdata/hold-geneseqg-embl/AA1984.DAT:*/SIDSI/gcgdata/hold-geneseqg-embl/AA1985.DAT:*/SIDSI/gcgdata/hold-geneseqg-embl/AA1985.DAT:*/SIDSI/gcgdata/hold-geneseqg-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-geneseqg-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-geneseqg-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-geneseqg/geneseqp-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-geneseqg/geneseqp-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-geneseqg/geneseqp-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-geneseqg/geneseqp-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-geneseqg/geneseqp-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-geneseqg/geneseqp-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-geneseqg/geneseqp-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-geneseqg/geneseqp-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-geneseqg/geneseqp-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-geneseqg/geneseqp-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-geneseqg/geneseqp-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-geneseqg/geneseqp-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-geneseqg/geneseqp-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-geneseqg/geneseqp-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-geneseqg/geneseqg-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-geneseqg/geneseqg-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-geneseqg/geneseqg-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-geneseqg/geneseqg-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-geneseqg/geneseqg/geneseqg-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-geneseqg/geneseqg/geneseqg/geneseqg-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-geneseqg/geneseqg/geneseqg-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-geneseqg/geneseqg/geneseqg/geneseqg/embl/AA1987.DAT:*/SIDSI/gcgdata/hold-geneseqg/geneseqg/embl/AA1987.DAT:*/SIDSI/gcgdata/hold-geneseqg/geneseqg/embl/AA1987.DAT:*/SIDSI/gcgdata/hold-geneseqg/geneseqg/geneseqg/embl/AA1987.DAT:*/SIDSI/geneseqg/embl/AA1987.DAT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /SIDSI/gcgdata/hold-geneseq/geneseqp-embi/waljuc.com./SIDSI/gcgdata/hold-geneseq/geneseqp-embi/walgg.ndT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embi/Aalgg0.baT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embi/Aalgg0.baT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MARYMLLLLLAVWVLTGELW......GLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 747574
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               747574 seqs, 111073796 residues
                                                                                                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A_Geneseq_032802;*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-781-077-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                                                 Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Human insulin homo Mouse insulin fami Mouse Zins3 protei Human Zins3 protei Pro-insulin-like p PRO182 polypeptide Human PRO182 prote Human insulin fami PRO182 Polypeptide Human EST encoded Human EST encoded
SUMMARIES	AAG78114 AAY95771 AAW37926 AAW37925 AAY01961 AAB00173 AAB00173 AAB04173 AAY95770 AAY95770 AAY95770 AAY94033 AAU12309
DB	22 19 20 20 21 21 21 22 22
% Query Match Length DB	142 135 135 135 135 135 135 135
% Query Match	100.0 19.5 19.3 16.6 16.6 16.6 16.6 16.6 16.6
Score	760 148 126.5 126.5 126.5 126.5 126.5 126.5 126.5
Result No.	11 110 110

34..47
/label- B_chain_consensus_sequence_region
/note= "Given in SEQ ID NO 3"
37..41
/label= B_chain_conserved_motif

Human immunostimul	Zins4. Zins4. mosome 19p13.11; cytostatic; ive disorder; prostate disorder; adal development; pregnancy; cadal development; pregnancy; tile tissue; cardiovascular disease; idothelial cell; osteoblast; tic balance; gene therapy. in d in claim 4" sisus_sequence_region	ID NO 3"
AAB52 AAP401 AAP401 AAP303 AAP303 AAP303 AAP401 AAP401 AAP401 AAP401 AAP401 AAP601 AAP602 AAR64 AAR64 AAR64 AAR67 AAR848 AAR848 AAR806 AAR	ALIGNN 142 AA. 142 AA. (in: chrome eproductive contraction contraction contraction) contraction; contraction; contraction; csmoth con csmoth contraction; claimed in claimed in consens	SEQ
252222222222222222222222222222222222222	ALIG sin; 142 AA. 'y) Polypeptide elaxin; chro is; reproduct is; reproduct se; ovarian ome, contrac 'myocyte; e ension; osmoi 'myocyte; e ension; osmoi 'myocyte; e ingal_peptid ature_protei ins4, claime _chain laimed in cl	lven in chain
1355 1855 1855 1855 1855 1855 1855 1855	dard; Protein; 142 AA (first entry) homologue polypeptid ; vasotropic; reproduc; ; vasotropic; reproduc; ; vasotropic; reproduc; ; vasotropic; reproduc; ; kidney disorder; go ; menopause; ovarian impotence; mocyte; ; muscle tension; osm Location/Qualifiers 125 1	
100 10 10 10 10 10 10 10 10 10 10 10 10	114 standard; Prot 114; 1-2001 (first ent; insulin homologue insulin; zins4; rrility; vasotropi disorder; kidney of al change; menopau stic ovarian syndr control; impotence ressure; muscle t tpiens. Location 11.25 7 label= n 7 note= 25 26.52 26.52 26.52 7 label= n 7 note= 7 74.47 74.47	3741 /label=
1126 11001 1001 1009 1009 1009 1009 1009 10	11 11 11 11 11 11 11 11 11 11	
1132 1132 1132 1132 1132 1132 1133 1133	RESULT 1 AAG78114 XX XX XAC AAG7811 XX X	Region
	RES AAG XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	

```
New insulin homologue polypeptide having homology to relaxin family, designated zins4 and zins4 polynucleotide, useful for diagnosing, preventing, treating reproductive, prostate, heart and kidney disorders
                                              /note= "Cleavage site at the junction of the C peptide and the A chain with a conserved RXXR motif"
                                                                                            /label= A_chain_consensus_sequence_region
/note= "Given in SEQ ID NO 5"
                                                                                                   /note= "Given in SEQ ID NO 4"
                                                                          /label= A_chain
/note= "Claimed in claim 2"
                                   "Claimed in claim 3"
                                                                                                                                                                                                                                                                Claim 6; Page 72-73; 79pp; English.
                                                                                                                                                                                          Jaspers SR;
                       'label= C_peptide
                                                                                                                                                09-FEB-2001; 2001WO-US04199.
                                                                                                                                                              10-MAR-2000; 2000US-0523346.
                                                                                                                                                                            (ZYMO ) ZYMOGENETICS INC.
                                                                  119..142
                                                                                         .142
                                              .118
                  118
                                         /note=
                                                                                                                                                                                           Holloway JL, Lok S,
                                                                                                                                                                                                          WPI; 2001-582454/65.
                                                                                                                                                                                                                 N-PSDB; AAH79088
                                                                                                                     WO200168862-A1.
                                               Cleavage-site
           Cleavage-site
                                                                                                                                    20-SEP-2001
                                                                                            Region
                                                                      Reqion
                     Region
                                   Region
```

```
The invention relates to an isolated insulin homologue zins4 having composition family. The zins4 gene, located on chromosome compositions as a lata amino acid protein, where the zins4 polypeptide 1913:11, encodes a 142 amino acid protein, where the zins4 polypeptide comprises a B chain and A chain comprising amino acid residues 26-52 and comprises a behain and A chain comprising amino acid residues 26-52 and comprises a betain a chain comprising and vasotropic activity. Zins4 has cytostatic, antifertility and vasotropic activity. Zins4 has cytostation in himmans and animals and in therapies for treating proteins are useful in applications for enhancing fertilisation during proteins are useful in treating suscell in treating reproductive assisted reproductive disorders and to identify cells, respect to the zins4 polypeptides and modulators of the inhibitors of its activity. Zins4 polypeptides and modulators of the inhibitors of its activity. Zins4 polypeptides and modulators of the inhibitors of its activity. Zins4 polypeptides and modulators of the inhibitors of its activity. Zins4 polypeptides and modulators of the contain syndrome and other reproductive function, ovulation, prostate, testicular cancer, fertility, ovarian function, ovulation, pathological conditions and only better the varian syndrome and other reproductive functions including concern the molecules are also useful for treating dysfunction associated concern the molecules are also useful for treating dysfunction, vivo, with contractile tissues or to suppress or enhance contractility in vivo, contractility in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 maturation of ovarian cells, myocytes, endothelial cells, osteoblasts in culture and in the study of the ovarian cycle, reproductive function, ovarian cell-cell interactions and fertilisation. The polypeptide is also useful as a modulator of blood pressure, muscle tension and osmotic balance. The zins4 polynucleotide is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        birth control, treating impotence or other male reproductive dysfunction, inducing birth, for promoting growth, differentiation, development and/or maturation of ovarian cells, myocytes, endothelial cells, osteoblasts in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 142 AA;
```

.. 9

1 MARYMLLLLLAVWVLTGELWPGAEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAH 60

ŏ

Gaps

0

100.0%; Score 760; DB 22; Length 142; 100.0%; Pred. No. 1e-74; tive 0; Mismatches 0; Indels 0;

Best Local Similarity 100. Matches 142; Conservative

Query Match

```
The present sequence is that of a murine paralog (see AAV95771) of munan zins3 (see AAV95770), a novel member of the insulin/relaxin cannot be munan zins3 (see AAV95770), a novel member of the insulin/relaxin cannot be made that more chromosome lassociated family member that maps to a region of human chromosome lassociated cannot be used converted (NIDDM). The sequence with non-insulin dependent diabetes mellitus (NIDDM). The sequence converted converted that mouse zins3 is expressed in chlots of embryo tissue indicated that mouse zins3 is expressed in chlots of embryo tissue indicated that mouse zins3 is expressed in collection of converted fashing. Zins3 polymorphisms that converted converted to a developmentally regulated fashing. In the human zins3 gene. The invention result from mutations in the human zins3 gene. The invention that provides methods for identifying abnormalities in expression that care a factor in causing, or predisposing, a person to some defect in glucose metabolism, such as NIDDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying mutations in human chromosome 1p31, preferably a zins3 gene mutation, comprises using an insulin/relaxin family member (designated zins3), useful for diagnosing non-insulin dependent diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51; Indels 36; Gaps
                                                                          61 EAMGDIEPDADADEDSLAGELDEAMGSSEWLALIKSPQAFYRGRPSWQGIPGVLRGSRDV 120
Lok S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jaspers SR, Whitmore TE, Conklin DC, Lofton-Day CE,
                                                                                                                                                                                                                                                                                                                                                                               non-insulin dependent diabetes mellitus; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.5%; Score 148; DB 21;
29.9%; Pred. No. 2.8e-08;
tive 21; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; Page 46-47; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                      Zins3; insulin; relaxin; mouse; NIDDM;
                                                                                                                                                                                                                                                                                                                                      Mouse insulin family homologue zins3.
                                                                                                                                                                                                                                              AAY95771 standard; Protein; 135 AA.
                                                                                                                                     121 LAGLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                          10-FEB-2000; 2000WO-US03515.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0198248.
99US-0250125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 29.9
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                07-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-558220/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAA50153
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200047776-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-AUG-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                     AAY95771;
                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                          Ω
                                                                                                                    g
                                                                                                                                                    ŏλ
                                                       g
                           Qγ
```

. 6

Gaps

51; Indels

Length 135;

19.3%; Score 147; DB 19; Conservative 21; Mismatches 51;

Local Similarity les 46; Conserv

Matches

ò Dp δ QQ οy

Query Match

1 MARYMLLLLLAVWVLTGELWPGAEARAAPYGVRLGGREFIRAVIFTGGSRWRRSDILAH 60

```
The Zins3 protein is an insulin homologue protein. Polynucleotide using an expression vector. The cell will express an insulin homologue cusing an expression vector. The cell will express an insulin homologue polypeptide encoded by the polynucleotide. The polypeptides can also be conhuman animal. The polypeptides can be used to identify and isolate ceptors for zins3. Antibodies and antagonists of the polypeptides can be used for treating disease associated with the polypeptide, such as reproductive disorders can sesociated with the polypeptide, such as reproductive disorders can associated with the placenta and uterus, gastrointestinal diseases placental and colon pathology. Antagonists against the polypeptide may can be used to treat diseases such as preclampsia, premature labour, and
                                 61 EAMGDIFPDADADEDSLAGELDEAMGSSEWL------ALTKSPQAFYRGRPSWQ 108
                                                 Insulin homologue polypeptide(s) and antagonists - used to, e.g. treat pre-eclampsia, premature labour and Crohn's disease
                                                                                                                                                                                                                                                            Insulin homologue; identification; isolation; Zins3 receptor; treatment; disease; pre-elampsia; premature labour; Human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lok S;
                                                                               109 GTPGVLRGSRDVLAGLSSSCCKWGCSKSEISSLC 142
                                                                                               106 lkkhsvvsrrd----lqalccregcsmkelstlc 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conklin DC, Jaspers SR, Lofton-Day CE,
                                                                                                                                                               AAW37926 standard; Protein; 135 AA.
                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                         /ucc.
49..115
"nte= "C-peptide"
                                                                                                                                                                                                                                                                                                                                                      "B chain"
                                                                                                                                                                                                                                                                                                                                                                                                    /note= "A chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 9; Page 67; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97WO-US18593.
                                                                                                                                                                                                              01-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96US-0028177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                             23..48
/note=
                                                                                                                                                                                                                                      Mouse Zins3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-251285/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAV29153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                               23-APR-1998.
                                                                                                                                                                                       AAW37926;
                                                                                                                                                                                                                                                                                                    Mus sp.
                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                          RESULT
          a
                                                        qq
                                                                               δ
                                                                                                     Db
```

```
The Zins3 protein is an insulin homologue protein. Polynucleotide

CC molecules taken from its gene can be introduced into a cultured cell

cusing an expression vector. The cell will express an insulin homologue

CC polypeptide enroded by the polynucleotide. The polypeptides can also be

CC combuman animal. The polypeptides can be used to identify and isolate

CC receptors for zins3. Antibodies and antagonists of the polypeptides can

CC receptors for zins3. Antibodies and antagonists of the polypeptides can

CC receptorated with the polypeptide, such as reproductive disorders

CC associated with the polypeptide, such as reproductive disorders

CC associated with the placenta and uterus, gastrointestinal diseases, and

CC placental and colon pathology. Antagonists against the polypeptide may

CC also be used to treat diseases such as preclampsia, premature labour, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insulin homologue polypeptide(s) and antagonists - used to, e.g. treat pre-eclampsia, premature labour and Crohn's disease
                                                                                                                     Insulin homologue; identification; isolation; Zins3 receptor;
treatment; disease; pre-elampsia; premature labour; Human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lok S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lofton-Day CE,
          AAW37925 standard; Protein; 135 AA.
                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                             Claim 2; Page 64-65; 81pp; English.
                                                                                                                                                                                                                         /note= "B chain"
                                                                                                                                                                                                                                                                             /note= "A chain"
                                                                01-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                              97WO-US18593.
                                                                                                                                                                                                                                                                                                                                                                                        96US-0028177.
                                                                                                                                                                                                                                                                                                                                                                                                             (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Jaspers SR,
                                                                                            Human Zins3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-251285/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAV29150
                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                  WO9816635-A1.
                                                                                                                                                                                                                                                                                                                                                        15-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                  15-0CT-1996;
                                                                                                                                                                                                                                                                                                                                23-APR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Conklin DC,
                                      AAW37925;
                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                              Peptide
AAW37925
```

135 AA;

Sequence

Matches

SXS

AAY01961

g

g ò

ΩD δŽ

```
86 dasgedriwg-----gqmpteelwkskkhsvmsrqd------iqtlcc 122
                                                                                                                                                                              71 DAD-EDSLAGELDEAMGSSEWLALTKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCC 129
                                                                                                           ---SDILAH-----EAMGDIFPDA 70
                                                                                                                                    Indels 45; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRO211; PRO228; PRO538; PRO172; PRO182; neoplasia; inhibition; tumour; treatment; therapy; agonist; antibody; breast cancer; ovarian cancer; renal cancer; colorectal cancer; uterine cancer; prostate cancer; lung cancer; bladder cancer; melanoma; leukaemia; prostate cancer; lung cancer; bladder cancer; immunologic disorder; inflammatory disorder; angiogenic disorder; immunologic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "CAMP- and cGMP-dependent protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Casein kinase II phosphorylation site"
                                        16.6%; Score 126.5; DB 20; Length 135; 30.8%; Pred. No. 6.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Insulin family signature
125.131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125..131
/note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "N-myristoylation site"
                                                                   30.8%; Preq. .... 8; Mismatches
                                                                                                                       32 VRLCGREFIRAVIFTCGGSRWRR-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Signal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                        AAB00173 standard; Protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0145698.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0131445.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US28564.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0123957
                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note=
                                                                                          41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                                   130 KWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                          ||| :::|:||
|123 tdgcsmtdlsalc 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRO182 polypeptide.
                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200055319-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modifled-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-JUL-1999;
08-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-APR-1999;
20-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB00173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Domain
             Sequence
                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human.
                                                                                                                                                                                                                                                                                                                                                                 RESULT AABOO173
                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                              δy
x os
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents an insulin-like polypeptide (pro-ILP). The protein is expressed in the colon and uterus, and is a member of the insulin/IGF family. The immature pro-ILP comprises a 135 maino of the insulin/IGF family. The immature pro-ILP comprises a 135 maino acid sequence, which is processed into the mature form which comprises and A chain and a brain linked by disulfide bonds. The C-peptide of pro-ILP exists as a separate peptide after processing of pro-ILP. The protein is useful in treatment of disorders related to ILP protein is useful in treatment of disorders related to ineurophysicological function affecting fluid homeostasis, electrolyte homeostasis, cardiovascular function, blood pressure, somatic or cardiac homeostasis, cardiovascular function, blood pressure, somatic or cardiac homeostasis, cardiovascular function, blood pressure, somatic or cardiac deposition. The methods can be used for diagnosing a physiologic or pathologic condition of the uterus, colon or other ILP-expressing cell pathologic condition of the uterus, colon or other ILP-expressing cell or tissue and for diagnosis and screening of modulators and therapeutics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Insulin-like polypeptide; pro-ILP; ILP; insulin/IGF family; A chain; B chain; C chain; neurophysiological function; fluid homeostasis; electrolyte homeostasis; cardiovascular function; blood pressure; somatic; cardiac innotropic activity; blood pressure; somatic; cardiac innotropic activity; cardiac chronotropic activity; collagen deposition.
                                                                                                                                                                                                                                  71 DAD-EDSLAGELDEAMGSSEWLALTKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCC 129
                                                                                                                                                                                                                                                                   86 dasgedriwg-----gqmpteelwkskkhsvmsrqd------iqtlcc 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Colon and uterus expressed insulin-like polypeptide, useful in the treatment of disorders related to neurophysiological function
                                                                                                                                                                 32 VRLCGREFIRAVIFTCGGSRWRR-----SDILAH-----EAMGDFFPDA 70
                                                                                                                                                                                          39; Indels '45; Gaps
                                                                                          16.6%; Score 126.5; DB 19; Length 135; 30.8%; Pred. No. 6.1e-06; tive 8; Mismatches 39; Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pro-insulin-like peptide (pro-ILP).
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY01961 standard; Protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 5; Fig 6B; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-US17888.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-0059836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1999 (first entry)
                                                                                                                              Local Similarity 30.8% les 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                         130 KWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                              ||| :::|:||
| 123 tdgcsmtdlsalc 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-254713/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAX35204
                                                             135 AA;
                          Crohn's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9915664-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gurney A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY01961;
                                                               Sequence
                                                                                                                   Query Match
```

```
Isolated PRO211, PRO228, PRO538, PRO172 or PRO182 polypeptides

or their agonists (preferably anti-PRO agonist antibody or a small

conclecule minicking the biological activity of PRO polypeptide) are

compositions comprising the biological activity of propertide) are

compositions comprising the PRO polypeptides are useful for tunibility meoplastic cell growth and for treating cancer including

contral nervous system cancer, uterine, prostate, lung, bladder,

contral nervous system cancer, melanoma and leukaemia in a mammal.

con the PRO polypeptides are also useful for treating other disorders

controphagal, epithelial, strocytal, hypothalamic and other glandular,

controphagal, epithelial, strocytal, lastococlic disorders and

continued processing the properties and menunologic disorders as well as being

controlled with a candidate molecule and monitoring biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, PRO, promotion; inhibition; angiogenesis; cardiovascularisation;
dlagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
anglogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;
cytostatic; gene therapy; vaccine.
                                                                                                Ashkenazi AJ, Goddard A, Gurney AL, Klein RD, Napier MA, 'Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 DAD-EDSLAGELDEAMGSSEWLALIKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86 dasgedriwg-----gqmpteelwkskkhsvmsrqd------19tlcc 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 VRLCGREFIRAVIFTCGGSRWRR-----SDILAH-----EAMGDTFPDA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 vrlcgleyirtviyicassrwrrhlegipqaqqaetgnsfqiphkrefseenpaqnlpkv 85
                                                                                                                                                                                            PRO211, PRO228, PRO538, PRO172 and PRO182 polypeptides useful for
                                                                                                                                                                                                                treating tumors including cancers of the breast and lung,
leukeamia and for identifying compounds capable of inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.6%; Score 126.5; DB 21; Length 135; 30.8%; Pred. No. 6.1e-06; tive 8; Mismatches 39; Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human PRO182 protein sequence SEQ ID NO:16.
                                                                                                                                                                                                                                                                              Claim 31; Fig 10; 133pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB24391 standard; Protein; 135 AA.
   99WO-US21090.
                 99WO-US23089.
                                     99WO-US28313.
                                                                                                                                                                                                                                              growth of neoplastic cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 30.89 hes 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-NOV-2000 (first entry)
                                                                 (GETH ) GENENTECH INC.
                                                                                                                                              WPI; 2000-638201/61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 KWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 tdgcsmtdlsalc 135
                                                                                                                                                                 N-PSDB; AAA54109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 135 AA;
 15-SEP-1999;
                                30-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200032221-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB24391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
```

```
The present invention describes nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing acadiovascular, endothelial or angiogenic disorder in mammals by acadiovascular, endothelial or angiogenic disorder in mammals by and for identifying agonists and antidonists of these processes. The conclete acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with anappropriate PRO expression such as cardiovascular, endothelial or angiogenic disorders in mammals (e.g. atherosclerosis, cancers and containing them and the PRO polypeptide may be used to treat disorders associated with decreased PRO expression. ANAT/310 to ANAT/321 and associated with decreased PRO expression. ANAT/310 to ANAT/321 and associated with decreased rule exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                              Goddard A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or anglogenic disorders in mammals -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39; Indels 45; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 VRLCGREFIRAVIFTCGGSRWRR------SDILAH-----EAMGDTFPDA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 vrlcgleyirtviyicassrwrrhlegipqaqqaetgnsfqlphkrefseenpaqnlpkv 85
                                                                                                                                                                                                                                                                                                                                                                                       Gerber H, Hillan KJ, Godda
Kuo SS, Paoni NF, Smith V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 21; Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   y Match
16.6%; Score 126.5; DB 2
Local Similarity 30.8%; Pred. No. 6.1e-06;
hes 41; Conservative 8; Mismatches 39
                                                                                                                                                                                                                                                                                                                                                                                       Asinkenazi AJ, Baker KP, Ferrara N,
Godowski PJ, Gurney AL, Klein RD, F
Watanabe CK, Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 72; Fig 8; 315pp; English.
                                               99WO-US28313.
                                                                                                                                                 99US-0131445.
                                                                                                                                                                              99WO-US12252.
                                                                            98WO-US25108
                                                                                                                                                                                                                          99US-0145698.
                                                                                                                       99WO-US05028
                                                                                                                                                                   99US-0134287
                                                                                                                                                                                                             99US-0144758.
                                                                                                                                                                                                                                        99WO-US20111.
                                                                                                                                                                                                                                                       99WO-US20594.
                                                                                                                                                                                                                                                                                             99WO-US21547.
99WO-US23089.
                                                                                                                                                                                             99US-0141037
                                                                                                                                                                                                                                                                 99WO-US20944
                                                                                                                                                                                                                                                                                  99WO-US21090
                                                                                                                                                                                                                                                                                                                            99US-0162506
                                                                                                                                                                                                                                                                                                                                                                                   Baker KP,
Gurney AL,
                                                                                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                         2000-412154/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAA77521
                                                                                                                                                                                                                                                                                                                                                                               Ashkenazi AJ,
                                          30-NOV-1999;
               08-JUN-2000.
                                                                        01-DEC-1998;
                                                                                                       :6661
                                                                                                                               2-MAR-1999;
                                                                                                                                                              4-MAY-1999;
                                                                                                                                                                         02-JUN-1999
                                                                                                                                                                                                                                                   08-SEP-1999;
                                                                                                                                                                                                                                                                                                                         29-OCT-1999;
                                                                                                                                                                                                                                                                 13-SEP-1999
                                                                                                                                                                                                                                                                                               15-SEP-1999
                                                                                                                    08-MAR-
                                                                                                    12-JAN-
                                                                                                                                                 28-APR-
                                                                                                                                                                                            23-JUN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

à q ò

130 KWGCSKSEISSLC 142 ||| :::|:|| |123 tdgcsmtdlsalc 135

```
The present sequence is that of zins3, a novel member of the insulin/relaxin family. The zins3 gene maps to human chromosome to insulin/relaxin family. The zins3 gene maps to human chromosome plain, a region that is correlated to a heritable form of non-insulin dependent diabetes mellitus (NIDDM). Zins3 mRNA is not expressed in detectable amnounts in healthy tissue, indicating that the zins3 in diabilitus (NIDDM). Zins3 mQND corresponding that the zins3 polynucleotides and polypeptides can specialized cell type. Zins3 polynucleotides and polypeptides can be used to diagnose disorders associated with abnormal expression of the zins3 protein, and to identify polymorphisms that result corresponds in the zins3 gene. In particular, the invention from mutations in the zins3 gene. In particular, the invention corresponding are a factor in causing, or predisposing, a person to some defect are a factor in causing, or predisposing, a person to some defect are a factor in causing, or predisposing, a person to some defect are a factor in involves cleavage at the C-terminus of the signal proper in involves cleavage at the C-terminus of the members of the insulin family, cleavage at the C-terminus of the remaining mand at the N-terminus of the A-chain, resulting in the N-terminus of the A-chain, resulting in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying mutations in human chromosome 1p31, preferably a zins3 gene mutation, comprises using an insulin/relaxin family member (designated zins3), useful for diagnosing non-insulin dependent diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               removal of the C-peptide. Cysteine residues at positions 29 and 41 (B-chain) and 121 and 125 (A-chain) are capable of associating through cysteine bridges and forming disulfide-bonded molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lok S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conklin DC, Lofton-Day CE,
                                                                                                                                                                Zins3; insulin; relaxin; human; diagnosis; NIIDM;
non-insulin dependent diabetes mellitus.
                                                                                                                                                                                                                                                                                           /label- Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 44-45; 51pp; English.
                                                                                                                                  Human insulin family homologue zins3.
                                                                                                                                                                                                                                                         Location/Qualifiers
                          AAY95770 standard; Protein; 135 AA.
                                                                                                                                                                                                                                                                                                                23..48
/label= B-chain
                                                                                                                                                                                                                                                                                                                                                              /label= C-chain
115..135
                                                                                                                                                                                                                                                                                                                                                                                                    /label= A-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-FEB-2000; 2000WO-US03515.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0198248.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0250125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jaspers SR, Whitmore TE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ZYMO ) ZYMOGENETICS INC.
                                                                                                    07-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-558220/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAA50150
                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200047776-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-FEB-1999;
                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                    AAY95770;
                                                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                      Peptide
 œ
                    AAY95770
RESULT
```

16.6%; Score 126.5; DB 21; Length 135;

Query Match

```
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Composition for inhibiting neoplastic cell growth and treating cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Klein RD, Napier M, Wood WI;
                                                                                               86 dasgedriwg-----gampteelwkskkhsvmsrqd------iqtlcc 122
                                                                          71 DAD-EDSLAGELDEAMGSSEWLALTKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCC 129
                                                                                                                                                                                                                                                                                       Inhibition; cancer; neoplasia; tumour; breast; ovary; renal; colorectal; uterus; prostate; lung; bladder; central nervous system; CNS; melanoma; leukaemia; PRO211; PRO228; PRO538; PRO172; PRO182;
                               32 VRLCGREFIRAVIFTCGGSRWRR------SDILAH------EAMGDTFPDA 70
                                                    26 vrlogleyirtviyloassrwrrhlegipqaqqaetgnsfqlphkrefseenpaqnlpkv 85
           45; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="cAMP and cGMP dependent protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Insulin family signature sequence"
Best Local Similarity 30.8%; Pred. No. 6.1e-06;
Matches 41; Conservative 8; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "N-myristoylation site" 127..131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96.102
/note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                  32..58 "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                /label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ashkenazi A, Goddard A, Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                      AAY83228 standard; Protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US23089.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0104080.
                                                                                                                                                                                                                                                     16-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113..117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
125..13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC
                                                                                                                               130 KWGCSKSEISSLC 142
                                                                                                                                           ||| :::|:||
|123 tdgcsmtdlsalc 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-317943/27.
                                                                                                                                                                                                                                                                            PRO182 Polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAZ93704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200021996-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-0CT-1998;
                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-APR-2000.
                                                                                                                                                                                                                                  AAY83228;
                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                      human.
                                                                                                                                                                                                    AAY83228
                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                    q
                                                                                                              g
                                                                                                                                   δλ
                                                                   q
                                                                                         δŏ
```

```
5,
 of ovary, uterus, prostate, lung and bladder, comprises PRO211, PRO228, PRO538, PRO172 or PRO182 polypeptide or their agonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides the protein and coding sequences of novel
                                                                                                                                                                                                                                                                                                                                                                  86 dasgedriwg-----gampteelwkskkhsvmsrqd------lqtlcc 122
                                                                                                                                                                                                             V Match 16.6%; Score 126.5; DB 21; Length 135; Local Similarity 30.8%; Pred. No. 6.1e-06; hes 41; Conservative 8; Mismatches 39; Indels 45; Gaps
                                                                                                                                                                                                                                                                                                                                    71 DAD-EDSLAGELDEAMGSSEWLALTKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCC 129
                                                                                                                                                                                                                                                                         32 VRLCGREFIRAVIFTCGGSRWRR------SDILAH------EAMGDTFPDA 70
                                                                                                                                                                                                                                                                                                     26 vrlcgleyirtviyicassrwrrhlegipqaqqaetgnsfqlphkrefseenpaqnlpkv 85
                                                                      Compositions comprising a PRO211, PRO228, PRO538, PRO172 or PRO182 POYPeptide or their agonists, mixed with a carrier is useful for inhibiting neoplastic growth and treating tumors such as cancers of breast, ovary, renal, colorectal, uterus, prostate, lung, bladder, central nervous system, melanoma and leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated polypeptide for treatment of diseases, diagnostics, raising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
diagnostics; forensic test; gene mapping; genetic disorder;
biodiversity; gene therapy; nutrition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qian XB, Wang Z, Chen R, Asundi V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human EST encoded protein SEQ ID NO: 1558.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang YT, Liu C, Zhou P, Qian XB, Wang
Cao Y, Drmanac RA, Zhang J, Werhman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; Page 1068-1069; 1275pp; English.
                                         Claim 14; Figure 10; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM24033 standard; Protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antibodies and research use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-JAN-2000; 2000US-0491404.
17-JUL-2000; 2000US-0617746.
03-AUG-2000; 2000US-0631451.
15-SEP-2000; 2000US-0663870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JAN-2001; 2001WO-US02687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                   130 KWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                        123 tdgcsmtdlsalc 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-476164/51.
                                                                                                                                                                     135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAH98692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200154477-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-AUG-2001.
                                                                                                                                                                    Sequence
                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM24033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10
                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM24033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
å
                                                                                                                                                                                                                                                                                                        d
                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

```
5.
proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomator. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, foremsics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy.
                                                                                                                                                                                                                                                             71 DAD-EDSLAGELDEAMGSSEWLALTKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCC 129
                                                                                                                                                                                                                                                                                       86 dasgedriwg-----gqmpteelwkskkhsvmsrqd-------1qtlcc 122
                                                                                                                                                                                        Gaps
                                                                                                                                                                                                        32 VRLCGREFIRAVIFTCGGSRWRR------SDILAH------EAMGDTFPDA 70
                                                                                                                                                                                                                                 26 vrlcgleyirtviyicassrwrrhlegipgaqqaetgnsfqlphkrefseenpaqnlpkv 85
                                                                                                                                                                                    39; Indels 45;
                                                                                                                                                       16.6%; Score 126.5; DB 22; Length 135; 30.8%; Pred, No. 6.1e-06; .ive 8; Mismatches 39; Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                            AAU12309 standard; Protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human PRO182 polypeptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2000; 2000WO-US32678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US28301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US28564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000WO-US04341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0170262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US30095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000WO-US04914.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US28551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US30911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US30999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000WO-US00277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000WO-US00376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000WO-US03565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000WO-US04342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000WO-US04414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000WO-US05004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000WO-US07532
2000WO-US08439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                               Best Local Similarity 30.898 Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000WO-US05601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000WO-US07377
                                                                                                                                                                                                                                                                                                                  130 KWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                            123 tdgcsmtdlsalc 135
                                                                                                              135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200140466-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-FEB-2000;
24-FEB-2000;
24-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAR-2000;
                                                                                                             Sequence
                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU12309;
                                                                                                                                                                                                                                                                                                                                                                                       RESULT
    8888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                    δλ
                                                                                                                                                                                                                                                                                                                                          q
```

```
ANULI72-AAU12446 represent novel human secretory and transmembrane

PRO polypeptides. The PRO polypeptides are useful to detect other

PRO polypeptides, to link bloactive molecules to cells expressing

PRO polypeptides, to modulate biological activities of cells expressing

PRO polypeptides, and to detect the presence of mammalian lung, colon,

PRO polypeptide expression in a cell sample to that in a control sample.

Come of the 275 sequences are also useful to stimulate the release of

Common necrosis factor-alpha (TMF-alpha) from human blood, the to

Come of the 275 sequences are also useful to stimulate the release of

Common necrosis factor-alpha (TMF-alpha) from human blood, the to

Come of the 275 sequences are also useful to stimulate the release of

Common necrosis factor-alpha (TMF-alpha) from human blood, the to

Come of the proliferation of chondrocytes, the proliferation or

Confidence to the proliferation of inner ear utricular supporting cells of

Confidence (PBMCs), or the proliferation of endothelial cells. Some of

Monocytes (PBMCs), or the proliferation of endothelial cells. Some of

Confidence may modulate glucose or free fatty acid uptake by

Skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide

Confidence or wind to binding interactions. The polynuclectides encoding

PRO Polypeptides can be used to generate probes, antisense RNA/DNA,

Confidence or wind to animals and can be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 DAD-EDSLAGELDEAMGSSEWLALTKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----lqtlcc 122
                                                                                                                                                                                Gao W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 VRLCGREFIRAVIFTCGGSRWRR-----SDILAH------EAMGDTFPDA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 vrlcgleyirtviyicassrwrrhlegipqaqqaetgnsfqlphkrefseenpaqnlpkv 85
                                                                                                                                                                                                                                                                                                                                      Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. lung, breast, prostate, cervical
                                                                                                                                                                              Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, G:
Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22; Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 6%; Score 126.5; DB 22; Length 30.8%; Pred. No. 6.1e-06; tive 8; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86 dasgedrlwg----gqmpteelwkskkhsvmsrqd-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB20110 standard; Protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 12; Fig 276; 813pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immunostimulant PRO182.
17-MAY-2000; 2000WO-US13705.
22-MAY-2000; 2000WO-US14042.
30-MAY-2000; 2000WO-US14941.
02-UNN-2000; 2000WO-US15264.
10-NOV-2000; 2000WO-US30873.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 30.8% hes 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 KWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||| :::|:||
|123 tdgcsmtdlsalc 135
                                                                                                                                            (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                   WPI; 2001-408281/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 135 AA;
                                                                                                                                                                                                                                                                                                         N-PSDB; AAS21381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB20110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB20110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      XEXEXEX
         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    пр
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
```

```
The present sequence is that of PRO182 (UNQ156), a novel human continuous degree of protein encoded by cDNA (see AAF30052) isolated from a uterine cDNA library. The invention provides polynuclectides from a uterine cDNA library. The invention provides polynuclectides compositions comprising these proteins or including PRO182. Claimed compositions comprising these proteins or their agonists are useful for increasing infiltration of inflammatory comprising a tissue of a mammal, stimulating or enhancing an immune crepionse in a mammal, or increasing the proliferation of T-lymphocytes in a mammal in response to an antigen. Claimed compositions in effect. A claimed method for treating an immune related disorder, comprising the PRO polypeptide or its antagonist have the opposite composition as a T cell disorder, involves administering the PRO polypeptide, such as an antagonist antibody. The disorder is selected from systemic lupus erythematosus, rheumatoid arthritis, csteparthris, juvenile chronic arthritis, spondyloarthropathy, csteparthris, juvenile chronic arthritis, spondyloarthropathy, csteparthris, systemic vasculitis, sarcoldosis, autoimmune haemolytic systemic vasculitis, sarcoldosis, autoimmune thrombocytopeania, thyroiditis, diabetes mellitus, cameamia, autoimmune thrombocytopeania, thyroiditis, diabetes mellitus, circhosis, granulommatous hepatitis, sclerosing cholangitis, cc biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease (ulcerative colitis and Crohn's disease), cc gluten-sensitive enteropathy, Whipple's disease, (auto)immune—mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ, Gurney AL;
Hillan KJ, Mark MR, Marsters SA, Pitti RM, Tumas D, Watanabe CK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New PRO polypeptides, nucleic acids and (ant)agonists, useful for diagnosing and treating immune-related disorders, such as multiple sclerosis, rheumatoid arthritis and diabetes -
                                                                                                                                                                                                                                                                  107..111
/note= "cAMP- and cGMP-dependent protein kinase
PROJ82; UNQ156; human; immune disease; autoimmune disease; antirheumatic; antiarthritic; antiinflammatory; antianaemic; immunosuppressive; antithyroid; antidiabetic; neuroprotective; hepatotropic; virucide; dermatological; antipsoriatic; antiallergic; immunostimulant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "insulin family signature"
                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                        'note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                "N-myristoylation site"
                                                                                                                                                                                                                                                                                                     phosphorylation site'
                                                                                                                                                                                                                                             /label= Mature_protein
                                                                                                                                                                                                      /label- Signal_peptide
                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; Fig 6; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0144758.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-MAR-2000; 2000WO-US06884.
                                                                                                                                                                                                                                                                                                                                                                                                                                       125..131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121..136
                                                                                                                                                                                                                                                                                                                                                                                                  96..102
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note=
                                                                                                                                                                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001-103149/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAF30052.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200105972-A1
                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-JUL-1999;
                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                               Protein
```

```
5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; anglogenesis-associated protein; PRO; endothelial cell growth; cardiac hypertrophy; cardiovascular disorder; endothelial disorder; anglogenic disorder; atherosclerosis; osteoporosis; hypertension; myocardial infarction; diabetic retinopathy; rheumatoid arthritis; Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer; Allahelmer's disease; Huntington's disease; stroke; drug screening;
                                                                                                                                                                                                                                                                                                                              DAD-EDSLAGELDEAMGSSEWLALTKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCC 129
                                                                                                                                                                                                                                                                                                                                                      skin diseases (such as bullous skin disease, erythema multiforme and psoriasis), allergic diseases (such as asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity and urticaria), immunologic aliseases of the lung and transplantation associated diseases (such as graft rejection and graft-versus-host disease) (all claimed). Claimed methods of diagnosing these disorders comprise detecting the level of expression of the PRO gene. Also claimed are a method activity of the PRO peptide, vectors, host cells and
                                                                                                                                                                                                                                                                     32 VRLCGREFIRAVIFTCGGSRWRR------SDILAH-----EAMGDTFPDA 70
                                                                                                                                                                                                                                                                                                 26 vrlcgleyirtviyicassrwrrhlegipqaqqaetgnsfqlphkrefseenpaqnlpkv 85
                                                                                                                                                                                                                                               45;
                                                                                                                                                                                                          16.6%; Score 126.5; DB 22; Length 135; 30.8%; Pred. No. 6.1e-06; Live 8; Mismatches 39; Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human angiogenesis-associated protein PRO182, SEQ 1D NO:41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB53072 standard; Protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene therapy; transgenic animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US21090.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000WO-US00219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US05028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0144758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0145698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US20111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US20594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US23089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US28313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US28409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0134287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US12252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0141037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US21547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US28564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US28565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                          41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         130 KWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                     123 tdgcsmtdlsalc 135
                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                 Sequence 135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200053753-A2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-DEC-1999;
02-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-NOV-1999,
                                                                                                                                     antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB53072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
                                                                                                                                                                                                                                                                                                                                71
                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4AB53072
   255555555555x&
                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                ă
                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

```
The invention relates to novel human anglogenesis-associated proteins designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding PRO proteins. The invention also relates to vectors and host cells comprising a PRO nucleic acid, the recombinant production of a PRO protein, PRO antibodies specific for a PRO protein, fusion proteins additionally encompasses methods of identifying modulators of PRO comprising a PRO protein, agonists or antaqonists of a PRO protein, and additionally encompasses methods of identifying modulators of PRO expression or activity; diagnoshing a cardiovascular, endothelial or angiogenic disorder, or a susceptibility to such a disorder by detecting mutations in a PRO gene, or the expression level of a PRO gene within a particular tissue; treating a cardiovascular, endothelial or angiogenic disorder via the administration of a PRO protein, PRO nucleic acid; and methods of inhibiting or stimulating endothelial cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the administration of a PRO protein, or an agonist or antagonist thereof. PRO nucleic acid; and methods of inhibiting or stimulating endothelial cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the administration of a PRO protein, or an agonist or antagonist thereof. PRO nucleic acid; and methods of inhibitime or stimulating endothelial or angiogenic disorders, such as a cardiovascular, production of PRO proteins, as hybridisation probes to screen libraries to isolate colds are additionally useful in the recombinant production of PRO proteins, to analyse genetic disorders, and in a cold and penes encoding PRO proteins, to analyse genetic disorders, and in a penes encoding PRO proteins, to analyse genetic disorders, and and in therapy. PRO nucleic acids are algebrate production of processing and processing of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              animals useful for the development and screening of potential therapeutic agents. The present sequence represents a PRO protein of the
                                                            Goddard A;
~~* MR, Marsters SA;
                                                                                                                                                                                                                                     New isolated nucleic acid for producing a PRO polypeptide, analyzing genetic disorders and treating cardiovascular, endothelial or anglogenic disorders, such as atherosclerosis, wounds or cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DAD-EDSLAGELDEAMGSSEWLALTKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----1qtlcc 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32 VRLCGREFIRAVIFTCGGSRWRR------SDILAH-----EAMGDTFPDA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16.6%; Score 126.5; DB 22; Length 135; 30.8%; Pred. No. 6.1e-06; tive 8; Mismatches 39; Indels 45;
                                                                         (P, Ferrara N, Gerber H, Goddard A,
NL, Hillan KJ, Kuo SS, Mark MR, Ma
Watanabe CK, Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86 dasgedrlwg-----gqmpteelwkskkhsvmsrgd----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAP40108 standard; Protein; 185 AA.
                                                                                                                                                                                                                                                                                                                                       Claim 69; Fig 18; 293pp; English.
                                                                      Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                         (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 KWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||| :::|:||
123 tdgcsmtdlsalc 135
                                                    Ashkenazi AJ, Baker
                                                                                                                         Pitti RM,
                                                                                                                                                                   WPI; 2001-090793/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 AA;
                                                                                                                                                                                             N-PSDB; AAC97396
                                                                                                                         Paoni NF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAP40108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAP40108
qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δŻ
```

ŝ

```
AAP94621
RESULT
                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The inventors claim a ds DNA SQ which comprises a coding strand and a complementary strand corresp. to (AAN40086) and its subunits. Also claimed are synthetic human H2-preprorelaxin, human H2-prorelaxin and human H2-relaxin together with their analogues having shortened A or B chains, or modified to contain different AA residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99 -----AFYRGRPS-----WQGTPGVLRGSRDVLAGLSSSCCKWGCSKSE 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MARYMLLLLLAVWVLTGELWPGAEARAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 EAMGDIFPDADADEDSLAGELDEAMGSSEWLA-----LIKS-----PQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene for expression of human H2-preprorelaxin - useful as vector for prodn. of the peptide after expression etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.7%; Score 111.5; DB 5; Length 185; 22.7%; Pred. No. 0.00038; ive 23; Mismatches 77; Indels 43;
                                                              Relaxin; hormone; probe; uterine contraction.
                                                                                                              Location/Qualifiers
                                      Sequence of human preprorelaxin H2
                                                                                                                                                                                                                                                                                                                                                                                                                 Tregear GW;
                                                                                                                                                                          58..161
/label= C-peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 2; 56pp; English.
                                                                                                                                                  25..57
/label= B-chain
                                                                                                                                                                                                  162..185
/label= A-chain
                                                                                                                                       /label= signal
                                                                                                                                                                                                                                                                                                             82AU-0007247.
83AU-0022283.
88EP-0110103.
                                                                                                                                                                                                                                                                                                                                                                FLOREY H INST EXPER.
HOWARD FLOREY INST.
                                                                                                                                                                                                                                                                                        83EP-0307553
                                                                                                                                                                                                                                                                                                                                                                                         HOWD-) HOWARD FLOREY INST.
              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 14.7%
Best Local Similarity 22.7%
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               Hudson PJ, Niall HD,
                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1984-160129/26.
N-PSDB; AAN40086.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FLOR-) FLOREY HOWA-) HOWARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138 ISSLC 142
                                                                                                                                                                                                                                                                                        12-DEC-1983;
                                                                                                                                                                                                                                                                                                                             09-DEC-1983;
01-JAN-1988;
             04-FEB-1992
                                                                                                                                                                                                                                                                 27 - JUN - 1984
                                                                                                                                                                                                                                        EP112149-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence
                                                                                                                         Peptide
                                                                                                                                                    Region
                                                                                                                                                                           Region
                                                                                                                                                                                                   Region
```

```
"H2" relaxin is deduced from a cDNA clone, has the general properties of a growth factor and is capable of altering nature of connective tissue and inducing smooth muscle contraction, specifically during labour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99 ------AFYRGRPS------WQGTPGVLRGSRDVLAGLSSSCCKWGCSKSE 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 EAMGDTFPDADADEDSLAGELDEAMGSSEWLA-----LTKS-----PQ------ 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MARYMLLLLLAVWVLTGELWPGAEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10; Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human H2-relaxin analogues - with shortened and/or modified A and/or B chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
14.4%; Score 109.5; DB 3
Best Local Similarity 22.7%; Pred. No. 0.00062;
Matches 42; Conservative 22; Mismatches 78
                                                                                                                       Amino acid sequence of human preprorelaxin H2.
                                                                                                                                                                                                                                                                 1..25
/label=Signal peptide
                                                                                                                                                               Relaxin; H2-relaxin; pubic symphysis.
                                                                                                                                                                                                                                            Location/Qualifiers
AAP94621 standard; protein; 185 AA.
                                                                                                                                                                                                                                                                                                        26..57
/label=B-chain
58..161
/label=C-peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hudson PJ, Trgear GW, Niall HD;
                                                                                                                                                                                                                                                                                                                                                                                    162..159
/label=A-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; ; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83EP-0110103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82AU-0007247.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (FLOR-) FLOREY H INST EXPER
                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1989-047874/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAN92483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138 ISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 larfc 185
                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-DEC-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-DEC-1982;
                                                                              21-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP303033-A.
                                          AAP94621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                         Peptide
```

4;

QY Db Oy Ob

Search completed: June 27, 2002, 16:08:08 Job time: 277 sec

		,	
·			
			÷ ,

```
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein – protein search, using sw model

June 27, 2002, 16:05:31; Search time 28.78 Seconds (without alignments) 120.515 Million cell updates/sec Run on:

US-09-781-077-2 760 1 MARYMLLLLIAVWVLTGELW......GLSSSCCKWGCSKSEISSLC 142 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

Total number of hits satisfying chosen parameters:

231628 seqs, 24425594 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

/cgn2_6/ptodata/2/laa/5A_COMB.pep:*
/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:* Issued_Patents_AA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description	Sequence 6, Appli					No No	Ş.	ce 1	10.	10,	14	92,	12.	12,	2.		, 7	Ħ	7	7,	5,	2,	7	4	13,		
SUMMARIES	ID	US-08-950-720A-6	US-08-950-720A-2	5464756-16	US-08-950-720A-12	5464756-18	5464756-20	5464756-15	US-08-950-720A-13	US-08-443-568B-10	PCT-US94-06997-10	US-08-950-720A-14	US-08-353-476-92	US-08-443-568B-12	PCT-US94-06997-12	US-09-201-226-2	US-08-905-267-2	US-09-314-051-2	US-08-950-720A-11	US-08-589-028-2	US-08-784-582-2	US-08-785-271-2	PCT-US95-08596-2	US-08-697-954-2	US-08-484-219-4	S	US-09-314-051-13	5464756-8
	DB		e	9	٣	9	9	9	٣	Н	S	m	~	-	S.	4	7	4	m	m	٣	4	Ŋ	4	0	7	4	9
	Query Match Length DB	135	135	30	185	162	164	53	185	77	17	101	40	150	150	134	188	188	110	110	110	110	110	1070	31	213	213	24
æ	Query Match	19.5	16.6	15.3	14.4	14.1	13.5	13.4	13.0	12.9	12.9	12.5	12.2	11.8	11.8	11.6	11.6	11.6	11.1	11.1	11.1	11.1	11.1		10.0	10.0	10.0	ø.
	Score	148	126.5	116	109.5	107.5	102.5	102	98.5	86	98	95	92.5	89.2	89.2	88.5	88.5	88.5	84.5	84.5	84.5	84.5	84.5	79.5		92	^	74.5
	Result No.	1	7	m	4	Ŋ	ø	7	æ	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27

12,	US-08-240-121-12		94	9.1	69	45
Sequence 12, Appl Sequence 12, Appl	US-07-989-844-12 US-08-161-044-12		94 94	9.5 1.0	69 9	4 4 4 4
28,	US-07-989-845-28	Н	94	9.1	69	42
_	PCT-US94-06997-14	S	25	9.3	71	41
Sequence 14, Appl	US-08-443-568B-14	Н	25	9.3	71	40
	US-08-353-476-90	N	33	9.3	71	39
Sequence 2, Appl:	PCT-US94-06997-2	S	29	6.3	71	38
Sequence 5, Appl.	US-08-484-219-5	7	29	9.3	71	37
Sequence 2, Appl	US-08-443-568B-2	٦	29	9.3	71	36
4	US-08-785-271-4	4	110	9.4	71.5	32
Sequence 4, Appli	US-08-784-582-4	m	110	9.4	71.5	34
	US-08-589-028-4	m	110	9.4	71.5	33
Sequence 19, Appl	US-09-479-453-19	4	174	9.5	72	32
19,	US-09-479-409-19	4	174	9.5	72	31
Sequence 19, Appl	US-08-911-853-19	m	174	9.5	72	30
Patent No. 5464756	5464756-10	φ	33	9.6	73	29
Patent No. 5464756	5464756-11	ø	32	9.6	73	28

ALIGNMENTS

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
ODERATING SYSTEM: DOS
SOFTWARE: FastSEX for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/950,720A
                                                                            APPLICANT: CONALIN, Darrell C.
APPLICANT: Lofton-Day, Catherine E.
APPLICANT: Lok, Si
APPLICANT: Jaspers, Stephen R.
TITLE OF INVENTION: INSULIN HOMOLOG
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                        ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
                 Sequence 6, Application US/08950720A Patent No. 6046028 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 96-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37,438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                            98102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; FRAGRENT 11E
US-08-950-720A-6
                                                                                                                                                                                                                                                                                      STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX:
```

Query Match

19.5%; Score 148; DB 3; Length 135;

```
71 DAD-EDSLAGELDEAMGSSEWLALTKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCC 129
                                                                                                                                                                                                                                 JAMES A.; YANGURA. DENNIS J.; VANDLEN, RICHARD L.; WILKINS,
JAMES A.; YANSURA, DANIEL G.
JAMES A.; SEQUENCES: AD COMPOSITIONS FOR THE
JUNEAR OF SEQUENCES: 42
JUNEAR OF SEQUENCES: 42
JUNEAR OF SEQUENCES: 42
JUNEAR OF SEQUENCES: 42
JUNEAR OF SEQUENCES: 347
JAPLICATION NUMBER: 01-701-1992
PRIOR APPLICATION DATE: 01-701-1992
PRIOR APPLICATION NUMBER: 347,550
JULIANG DATE: 04-MAY-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                              86 DASGEDRIMG-----GOMPIEELWKSKKHSVMSRQD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.3%; Score 116; DB 6;
86.4%; Pred. No. 8.8e-07;
tive 3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SUSTUARRE: FASTSEO FOI Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/950,720A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: CONKlin, Darrell C.
APPLICANT: Lofton-Day, Catherine E.
APPLICANT: Lofk, Si.
APPLICANT: Jaspers, Stephen R.
ITILE OF INVENTION: INSULIN HOMOLOG
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/08950720A Patent No. 6046028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 37.438
REFERENCE/DOCKET NUMBER: 96-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 GIKLCGREFIRAVIYTCGGSRW 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31 GVRLCGREFIRAVIFTCGGSRW 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Sawislak, Deborah A REGISTRATION NUMBER: 37,4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                       130 KWGCSKSEISSLC 142
                                                                                                                                 123 TDGCSMTDLSALC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-950-720A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                    5464756-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                셤
                                                                                         Óγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δy
                            9
                                                                                                                                                                               61 EAMGDTFPDADADEDSLAGELDEAMGSSEWL------ALTKSPQAFYRGRPSWQ 108
                                                                                            1 MARYMLLLLLAVWVLTGELWPGAEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----SDILAH-----EAMGDTFPDA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.6%; Score 126.5; DB 3; Length 135; 30.8%; Pred. No. 3.9e-07; tive 8; Mismatches 39; Indels 45
                          51; Indels
    29.9%; Pred. No. 1.3e-09; tive 21; Mismatches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/950,720a
                                                                                                                                                                                                                                      109 GTPGVLRGSRDVLAGLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Conklin, Darrell C.
APPLICANT: Lofton-Day, Catherine E.
APPLICANT: Lok, Si
APPLICANT: Jaspers, Stephen R.
TITLE OF INVENTION: INSULIN HOMOLOG
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32 VRLCGREFIRAVIFTCGGSRWRR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 96-09
                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08950720A
Patent No. 6046028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37,438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 206-442-6672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Sawislak, Deborah A REGISTRATION NUMBER: 37,43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 30.8
Matches 41; Conservative
                          46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
Best Local Similarity
Matches 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER:
                                                                                                                                                                                                                                                                                                                                                              US-08-950-720A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-950-720A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                  δy
                                                                                                                                                                                            В
                                                                                                                                                                                                                                      δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δλ
```

Gaps

;; 0

```
4
                                                                                                                                                                                                                                                                                                                                                 61 DAPOTPRRVAEIVPSFINKDTETINMMSEFVANLPQELKLTLSEMQPALPQLQQHVPVLK 120
                                                                                                                                                                                                                                                                                                                                                                                                            121 DSSLLFEEFKKLIRNRQSEAADSSPSELKYLGLDTHSRKKRQLYSALANKCCHVGCTKRS 180
                                                                                                                                                                                                                                                                                                                                                                                99 ------AFYRGRPS------WQCTPGVLRGSRDVLAGLSSSCCKWGCSKSE 137
                                                                                                                                                                                                                                   78; Indels 43; Gaps
                                                                                                                                                                                                                                                     1 MARYMLLLLLAVWVLTGELWPGAEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAH 60
                                                                                                                                                                                                                                                                           61 EAMCDTFPDADADEDSLAGELDEAMGSSEWLA-----LTKS-----PQ------98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 14.1%; Score 107.5; DB 6; Length 162;
Local Similarity 23.4%; Pred. No. 7.6e-05;
hes 36; Conservative 20; Mismatches 55; Indels 43; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 ANLPQELKLTLSEMQPALPQLQQHVPVLKDSSLLFEEFKKLIRNRQSEAADSSPSELKYL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 VRLCGREFIRAVIFTCGGSRWRRSDILAHEAMGDTFPDADADBDSLAGELDEAMGSSEWL 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.4%; Score 109.5; DB 3; Length 185; 22.7%; Pred. No. 5.3e-05; tive 22; Mismatches 78; Indels 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: HENNER, DENNIS J.; VANDLEN, RICHARD L.; WILKINS, JAMES A.; YANSURA, DANIEL G.
TITLE OF INVENTION: PROCESS AND COMPOSITIONS FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PATENT NO. 5464756; PATENTER, DENNIS J.; VANDLEN, RICHARD L.; WILKINS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 GTPGVLRGSRDVLAGLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 GLDTHSRKKRQLYSALANKCCHVGCTKRSLARFC 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/07/908,766
FILING DATE: 01-JUL-1992
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: 347,550
FILING DATE: 04-MAY-1989
                          INFORMATION FOR SEQ ID NO: 12:
                                                                                          STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: No. 6046028e US-08-950-720A-12
                                         SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
                                                                                                                                                                                                                       42; Conservative
TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISOLATION HUMAN RELAXIN
NUMBER OF SEQUENCES 42
CURRENT APPLICATION DATA
                                                                               amino acid
                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                138 ISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 LARFC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Patent No. 5464756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 162
                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO:18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
5464756-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5464756-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5464756-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                     οy
                                                                                                                                                                                                                                                                                                                                               Ω
                                                                                                                                                                                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
```

```
ô
                                                                                                                                                                                                                                                                                                                                                                                                             82 DEAMGSSEWLALTKSPQA-----W 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                69 VANLPQELKITLSEMQPALPQLQQHVPVLKDSSLLFEEFKKLIRNRQSEAADSSPSELKY 128
                                                                                                                                                                                                                                                                                                                                                                 32 VRLCGREFIRAVIFTCGGSRWRRSDILAHEAMGDT------FPDADADEDSLAGEL 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                          13.5%; Score 102.5; DB 6; Length 164; 22.4%; Pred. No. 0.00029; tive 20; Mismatches 56; Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.4%; Score 102; DB 6; Length 29; 81.0%; Pred. No. 3.4e-05; tive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: HENNER, DENNIS J.; VANDLEN, RICHARD L.; WILKINS,
JAMES A.; YANSURA, DANIEL G.
TITLE OF INVENTION: PROCESS AND COMPOSITIONS FOR THE
ISOLATION HOMAIN RELAXIIN
NUMBER OF SEQUENCES: 4.2
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JAMES A.; YANGGRA, DANIEL G.
TITLE OF INVENTION: PROCESS AND COMPOSITIONS FOR THE:
I ISOLATION HUMAN RELAXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 QGTPGVLRGSRDVL-AGLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 LGLDTHSRKKRDQLYSALANKCCHVGCTKRSLARFC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 42
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/908,766
FILING DATE: 01-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NATA:
APPLICATION NUMBER: 347,550
FILING DATE: 04-MAY-1989
                                                                                      APPLICATION NUMBER: US/07/908,766
FILING DATE: 01-UU-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 347,550
FILING DATE: 04-MAY-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Jaspers, Stephen R.
TITLE OF INVENTION: INSULIN HOMOLOG
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Conklin, Darrell C.
APPLICANT: Lofton-Day, Catherine E.
APPLICANT: Lok, Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 13, Application US/08950720A
; Patent No. 6046028
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZymoGenetics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 GVRLCGREFIRAVIFTCGGSR 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                      Best_Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
 ; JAMES A.; YANSURA,
                                                                                                                                                                                                   ; LENGTH: 164
5464756-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5464756-15
;Patent No. 5464756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-950-720A-13
                                                                                                                                                                             ; SEQ ID NO:20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17;
                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO:15
                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5464756-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                             δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
```

```
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 DSNLSFEBFKKLIRNROSEBADSNPSELKYLGLDTHSQKKRRPYVALFEKCCLIGCTKRS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 DAPOTPRPVABIVPSFINKDTETIIIMLEFIANLPPELKAALSERQPSLPELQQYVPALK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95 KSPQAF----YRGRPS-----WQGTPGVLRGSRDVLAGLSSSCCKWGGSKSE 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 13.0%; Score 98.5; DB 3; Length 185; Local Similarity 23.8%; Pred. No. 0.00098; Indels 43; Gaps ns 44; Conservative 19; Mismatches 79; Indels 43; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MARYMLLLLLAUWVLTGELWPGAEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MPRIELFFHLLEFCLLLNOFSRAVAAKWKDDVIKLCGRELVRAOIAICGMSTWSKRSLSQE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 EANGDIFFDAD-----ADEDS-----ALT 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Breece, Tim
APPLICANT: Breece, Tim
APPLICANT: Hayenga, Kirk
APPLICANT: Rindersknecht, Ernst
APPLICANT: Vandlen, Richard
APPLICANT: Vandlen, Richard
APPLICANT: Daniel, Yansura
TITLE OF INVENTION: Process for Producing Relaxin
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                 OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/950,720A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application US/08443568B Patent No. 5759807 GENERAL INFORMATION:
                      1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 96-05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEPAX: 206-442-6678
TELEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: No. 6046028e
                                                                                                                                                                                                                                                                                                                                                                    NAME: Sawislak, Deborah A REGISTRATION NUMBER: 37,43
                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 LAKYC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138 ISSLC 142
                                                 Seattle
                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-443-568B-10
                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-950-720A-13
                                                                                                    98102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

```
12.9%; Score 98; DB 1; Length 77;
19.8%; Pred. No. 0.00035;
Live 14; Mismatches 23; Indels 52; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32 VRLCGREFIRAVIFTCGGSRWRRSDILAHEAMGDTFPDADADEDSLAGELDEAMGSSEWL 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92 ALTKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42 ---RRPTGYGSGK-------KRQLYSALANKCCHVGCTKRSLARFC 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application PC/TUS9406997
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: 460 Point San Bruno Boulevard
APPLICANT: South San Francisco, California
APPLICANT: United States of America
APPLICANT: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                               JAROLIM TYPES: Floppy disk
COMPUTER: ISM PC COMPACTALE
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING PACTALIN Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 IKLCGRELVRAQIAICGMSTWSK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
12.9%; Score 5%; Obs. 18.0%; Match
Bast Local Similarity 19.8%; Pred: No. 0.00
Bast ches 22; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Pennie & Educusor STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US94/06997
FILING DATE: 20-JUN-1994
                                                                                                                            APPLICATION NUMBER: US/08/443,568B
FILING DATE: 22-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                           7842-037
                                                                                                                                                FILING DATE: 22-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA: 08/080,354
PILING DATE: 21-JUNE-1993
FILING DATE: 21-JUNE-1993
ATTORNEY/AGENT INFORMATION:
NAME: ADEAms, Samuel B.
REGISTRATION NUMBER: 30,605
                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 7842
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-5556
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: PROMISER OF SEQUENCES: 3 CORRESPONDENCE ADDRESS:
                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-08-443-568B-10
           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New York
U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U
10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGIH:
```

```
Gaps
                                                                                                                                                   33 RLCGREFIRAVIFTCGGSRWRRSDILAHEAMGDTFPDADADEDSLAGELDEAMGSSEWLA 92
                                                                                                                                                                       Gaps
                                                                                                                                                                                                            93 LTKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCCKWGCSKSEISSLC 142
                                                                                             ch 12.5%; Score 95; DB 3; Length 101; 24; Conservative 14; Mismatches 30; Indels
                                                                                                                                                                                                                                        65 -----PQTSHHH-------RHHRAAATNPAKYCCLSGCTQQDLLILC 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.2%; Score 92.5; DB 2; Length 40; 52.9%; Pred. No. 0.00065; Indels 1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Weininger, Susan
APPLICANT: Weininger, Arthur M
TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
NUMBER OF SEQUENCES: 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Rclease #1.0, Version #1.25
APPLICATION NUMBER: US/08/353,476
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Sallwanchik & Saliwanchik
STREET: 2421 N.W. 41st St., Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 PGAEARAAPYGVRLCGREFIRAVIFTCGGSRWRR 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 PNWEERS-----RLCGRDLIRAFIYLCGGTRWTR 30
                                                                                                                                                                                                                                                                                                                Sequence 92, Application US/08353476
Patent No. 5871902
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Bencen, Gerard H.
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: GP-1C
TELEBOOMUNICATION INFORMATION:
TELEBAX: (904) 375-8100
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity.
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                               US-08-950-720A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S
N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; FRAGMENT TYPE:
US-08-353-476-92
                                                                                                                                                                                                                                                                                                   US-08-353-476-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-443-568B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
                                                                                                                                                   δ
                                                                                                                                                                               q
                                                                                                                                                                                                            ά
                                                                                                                                                                                                                                      QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                         23; Indels 52; Gaps
                                                                                                                                                                                                                                                                                 32 VRLCGREFIRAVIFICGGSRWRRSDILAHEAMGDIFPDADADEDSLAGELDEAMGSSEWL 91
                                                                                                                                                                                                                                                                                                        19 IKLCGRELVRAQIAICGMSTWSK------41
                                                                                                                                                                                                                                                                                                                                            92 ALTKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                   ch 12.9%; Score 98; DB 5; Length 77; 18:milarity 19.8%; Pred. No. 0.00035; 22; Conservative 14; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/950,720A
                                7842-025-228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Conklin, Darrell C.
APPLICANT: Lofton-Day, Catherine E.
APPLICANT: Lofk, Si
APPLICANT: Jaspers, Stephen R.
ITLE OF INVENTION: INSULIN HONOLOG
CORRESPONDENCE ADDRESS:
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7842-(
TELECOMMUNICATION INPORMATION:
TELEPHONE: 415-684-3660
TELERAX: 6114 PENNIE
INPORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS: CENTRE OF TELEPHONE CONTRIBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEE: ZymoGenetics, Inc.: 1201 Eastlake Avenue East
Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/08950720A
Patent No. 6046028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Savislak, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 96-
TELECOMMUNICATION INFORMATION:
                                                                                                                     LENGTH: 77 amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: No. 6046028e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 101 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-950-720A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                              Ω
                                                                                                                                                                                                                                                                                                                                            δy
                                                                                                                                                                                                                                                                                                                                                                      q
```

Sequence 12, Application US/08443568B

```
113 VLRGSRDVLAGLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 HSRKKRQLYSALANKCCHVGCTKRSLARFC 150
                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REGISTRATION NUMBER: 7842-025-228
REFERENCE/DOCKET NUMBER: 7842-025-228
TELECPHONICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEPHONE: 415-854-3694
      3: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                          20-JUN-1994
20-JUN-1994
N:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
CRGANISM: Drosophila melanogaster
US-09-201-226-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-201-226-2

'Sequence 2, Application US/09201226

; Sequence 2, Application US/09201226

; Patent No. 6135942
                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415-854-3694
TELEFX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 22.7% Local Similarity 22.7% hes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                      New York
RY: U.S.A.
10036
                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                        New York
                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-US94-06997-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 ----LTKS-----PQ-----PQGTPG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 QELKLTLSEMQPALPQLQQHVPVLKDSSLLFEEFKKLIRNRQSEAADSSPSELKYLGLDT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GRELVRAQIALCGMSTWSKRSLSQEDAPQTPRPVAEIVPSFINKDTETINMMSEFVANLP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 11.8%; Score 89.5; DB 1; Length 150; Best Local Similarity 22.7%; Pred. No. 0.008; Matches 34; Conservative 18; Mismatches 55; Indels 43; Gaps Matches 34; Conservative 18; Mismatches 55; Indels 43; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36 GREFIRAVIFTCGGSRWRRSDILAHEAMGDTFPDADADEDSLAGELDEAMGSSEWLA--- 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Genentech, Inc.
APPLICANT: Genentech, Inc.
APPLICANT: 460 Point San Bruno Boulevard
APPLICANT: Outh San Francisco, California
APPLICANT: United States of America
TITLE OF INVENTION: Process for Producing Relaxin
NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,568B
FILING DATE: 22-MAY-1995
                                                                                                                                                         Process for Producing Relaxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 VLRGSRDVLAGLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12, Application PC/TUS9406997
GENERAL INFORMATION:
                                                                                                                                                                                                                        E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7842-037
                                                                                                                                                                                                                                                                                                                                         COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: BM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATING
                                                                      APPLICANT: Breece, Tim
APPLICANT: Hayenga, Kirk
APPLICANT: Rindersknecht, Ernst
APPLICANT: Vandlen, Richard
APPLICANT: Daniel, Yansura
TITE OF INVENTION: Process for Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 4.35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08,080,354
FILING DATE: 21-JUNE-1993
CLASSIFICATION: 4.35
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 650-493-5956
TELEFAX: 650-493-5556
TELEFAX: 65141 PENNIE
TELEX: REGIAL PENNIE
TELEX: SECUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 150 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Abrams, Samuel B. REGISTRATION NUMBER: 30,605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 78.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: protein US-08-443-568B-12
                                                                                                                                                                                          NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                     New York
                                                                                                                                                                                                                                                                                                           U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                    New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT-US94-06997-12
                                              Patent No. 5759807
                                                                                                                                                                                                                                                                                                                         10036
                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

```
4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 11.6%; Score 88.5; DB 4; Length 134; Best Local Similarity 25.5%; Pred. No. 0.009; Matches 37; Conservative 19; Mismatches 60; Indels 29; Gaps Matches 37; Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 QELKLILSEMQPALPQLQQHVPVLKDSSLLFEEFKKLIRNRQSEAADSSPSELKYLGLDT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 ----LTKS-----PQ------WQGTPG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55; Indels 43; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GRELVRAQIAICGMSTWSKRSLSQEDAPQTPRPVAEIVPSFINKDTETINMMSEFVANLP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 GREFIRAVIFTCGGSRWRRSDILAHEAMGDTFPDADADEDSLAGELDEAMGSSEWLA--- 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DETECT NO. VELLANDER OF A D. MELANOGASTER APPLICANT: LEPTIN, MATIA AND USES THEREOF TITLE OF INVENTION: INSULIN-LIKE GENE AND USES THEREOF TITLE OF INVENTION: LOS OF TITLE OF TABLE OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.8%; Score 89.5; DB 5; Length 150; 22.7%; Pred. No. 0.008; 55; Indels 43. tive 18; Mismatches 55; Indels 43.
COMPUTER: IEM PC Compatible
COMPUTER: PAPEL PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 7326-077
CURRENT APPLICATION NUMBER: US/09/201,226
CURRENT FILING DATE: 1998-11-30
CURRENT FILING DATE: 1998-11-30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
```

Search completed: June 27, 2002, 16:08:44 Job time: 193 sec

	•

•

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

June 27, 2002, 16:05:56; Search time 36.01 Seconds (without alignments) 378.914 Million cell updates/sec Run on:

US-09-781-077-2 760 Perfect score: Title:

1 MARYMLLLLLAVWVLTGELW......GLSSSCCKWGCSKSEISSLC 142 BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		- spir	1	2 prec	N	c	-			·H	relaxin precursor		relaxin precursor	relaxin 1 precurso	relaxin - dog (fra	insulin-related pr	relaxin 'gorilla	ø	cur	insulin precursor	hypothetical prote	insulin precursor	conserved hypothet	7	relaxin - minke wh	insulin precursor	insulin precursor	pristinamycin I sy	tin B,C and	txpc protein - Myc
SUMMARIES																															
SUM	Ð		PYPKOT	ACODOS	70000	242/86	7576	A20504	A34930	B53034	240004	44550	C - 440	COLUNA	342/03	6/00/0	*****	342/04	TDHU	442170	182119	100178	907004	10001	11009/ B32201	102200	D421/9	TAR	130288	T14182	
	DB			-	10	7 ~	10	1 0	۹ ۸	۰,	10	- 1	, ۱	1 0	٥ د	۱ د	٠,	۱ د	-, د	10	٠,	۱ ۸	٠,	, c	۰,	٠,	۹ -	٦ ,	4 (· ~	
	Length	54	44	185	166	182	131	187	199	131	185	185	186	166	9 5	145	57	178	110	110	139	110	106	187	5.4	110	116	2591	143	2129	
dР	Query	20.1	15.4	14.4	14.3	14.0	13.4	13.4	13.2	13.0	13.0	13.0	12.9	12.6	11.8	11.6	11.4	11.4	11.1	11.0	10.9	10.6	10.5	10.5	10.3	10.3	10.3	10.3	10.1	10.1	
	Score	153	117	109.5	108.5	106.5	102	101.5	100.5	66	66	98.5	86	95.5	89.5	88	86.5	86.5	84.5	83.5	82.5	80.5	80	80	78.5	78.5	78	78	77	77	
	Result No.	1	7	3	4	ស	9	7	89	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	

relaxin - sand tiger (tentative sequence) (fragments)
C; Species: Odontaspis taurus (sand tiger)
C; Accession: A01616
R; Gowan, L.K.; Reinig, J.W.; Schwabe, C.; Bedarkar, S.; Blundell, T.L.
R; Gowan, L.K.; Reinig, J.W.; Schwabe, C.; Bedarkar, S.; Blundell, T.L.
A; Title: On the primary and tertiary structure of relaxin from the sand tiger shark
A; Reference number: A01616; MUID:82004703

peptide synthetase relaxin - horse (finsulin precursor insulin precursor conserved hypothet transcription regulypothetical protection probable zinc meta probable zinc meta probable zinc meta probable zinc meta catalase (EC 1.11. relaxin - Bryde's insulin precursor insulin precursor
114164 A39883 A39883 IPHF IPHF RGECA171 F90866 C85752 A75849 A75849 A75849 A75840 A758
110000000000000
2569 108 115 115 380 513 513 513 193 663 576 576 107
100.1 100.1 100.1 100.1 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0
77 76.5 76.5 76.5 76.5 76.5 76.5 76.5 76
00000000000000000000000000000000000000

ALIGNMENTS

RESULT 1 A56463 A56463 C: Species: Squalus acanthias (spiny dogfish) C: Accession: 85463; A26463 Bur. J. Biochem. 161, 335-341, 1986 A77111er Isolation, purification and the sequence of relaxin from spiny dogfish (s. A77111er Isolation), purification and the sequence of relaxin from spiny dogfish (s. A77111er) A77111er Isolation, purification and the sequence of relaxin from spiny dogfish (s. A771111) A77111er Isolation, purification and the sequence of relaxin from spiny dogfish (s. A7711111) A771111er Isolation, purification and the sequence of relaxin from spiny dogfish (s. A7711111) A7711111 A77111111 A7711111111111111111
26463 26463 26463 26464 26464 2612 26463 2622510nnn 2622510nnnn 2622510nnnn 2622510nnnnn 27111ennnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
RESULT 1 A26463 relaxin - C;Species: 0;Date: 19 C;Aucessio R;Bullesba Bur. J. Bi A;Referenci A;Referenci A;Referenci A;Residues: A;Residue

us-09-781-077-2.rpr

```
A. Residues: 1-182 <HAL>
A. Residues: 1-182 <HAL>
A. Cross-references: GB:K01088; NID:g164634; PIDN:AAA31114.1; PID:g164635
A. Cross-references: GB:K01088; NID:g164634; PIDN:AAA31114.1; PID:g164635
B:James, R.; Niall, H.; Kwok, S.; Bryant-Greenwood, G.
Nature 267, 544-546, 1977
A. Title: Primary structure of porcine relaxin: homology with insulin and related grow A; Reference number: A93187; MUD:77213067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 18-Jun-1999
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1983 #text_change 18-Jun-1999
C;Accession: Ap0934; A93187; A90205; A90196; S32313; S32312; A29796; A01615
R;Haleson: Ap0934; A93187; Scanlon, D.; John, M.; Cronk, M.; Shine, J.; Tregear, G.; Ni DNA 1, 155-162, 1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 ANLPOELKLILSEMOPALPOLQOYVPVLKDSSLLFEEFKKLIRNRQSEAADSSPSELKYL 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Pan troglodytes (chimpanzee)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: EMBL: Z27245; NID: 9416109; PIDN: CAA81758.1; PID: 9416110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 VRLCGREFIRAVIFTCGGSRWRRSDILAHEAMGDTFPDADADEDSLAGELDEAMGSSEWL 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 IKLCGRELVRAQIALCGKSTWSKRSLSQEDAPQTPRPVAEIVPSFINKDTETINMMSEFV 72
                                                                                                                                                                                                                                                 121 DSSLLFEEFKKLIRNRQSEAADSSPSELKYLGLDTHSRKKRQLYSALANKCCHVGCTKRS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                61 DAPQTPRPVAELVPSFINKDTETINMMSEFVANLPQELKLTLSEMQPALPQLQQHVPVLK 120
                                                                                                                                                                 ------AFYRGRPS------WQGTPGVLRGSRDVLAGLSSSCCKWGCSKSE 137
61 EAMGDIFPDADADEDSLAGELDEAMGSSEWLA-----LIKS-----PQ----- 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92 A-----LTKS-----PQ-------AFYRGRPS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;1-5/Domain: signal sequence (fragment) #status predicted <SIG>F;6-166/Product: relaxin 2 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA 1, 155-162, 1982
A;Title: Porcine relaxin: molecular cloning and cDNA structure.
A;Reference number: A90934; MUID:83157118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 14.3%; Score 108.5; DB 2; Length : Best Local Similarity 23.4%; Pred. No. 0.0031; Matches 36; Conservative 20; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, November 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 GLDTHSRKKRQLYSALANKCCHVGCTKRSLARFC 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109 GTPGVLRGSRDVLAGLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein
A; Residues: 25-50, TWGR';161-182 <JAM>
R;Schwabe, C.; McDonald, J.K.; Steinetz, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       relaxin 2 precursor - chimpanzee (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: S42776
A; Accession: S42786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-166 <EVA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: A90934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession: S42786
R; Evans, B.B.
                                                                                                                                                                                                                                                                                                                                                                               138 ISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 LARFC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: rlx2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Óγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                  QY
                                                                                                                                                                                                                                                                                                                                                                                        δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Molecule type: protein
A, Residues: 25-53;162-185 <STU>
C;Genetics:
C;Genetics:
C;Genetics:
C;Genetics:
D9:RLN2
A, Gene: GDB:RLN2
A, Gene: GDB:RLN2
A, Consarreferences: GDB:RL953; OMIM:179740
A, Map position: 9pter-9q12
C;Superfamily: insulin
C; Superfamily: insulin
C; Superfamily: squence #status predicted <SIG>
F;12-4/Domain: relaxin 2 chain B #status experimental <BCH>
F;25-53, Momain: relaxin 2 chain B #status experimental <MAT>
F;25-53, Momain: relaxin 2 connecting C peptide #status predicted <CPEP>
F; 88-157/Domain: relaxin 2 chain A #status experimental <ACH>
F; 81-172, A7-185, 171-176/Disulfide bonds: #status experimental
F; 15-172, A7-185, 171-176/Disulfide bonds: #status experimental
F; 162, Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: GB:X00948; NID:g35926; PIDN:CAA25460.1; PID:g35927
R; Stults, J.T.; Bourell, J.G., Canova-Davis, E.; Ling, V.T.; Laramee, G.R.; Winslow, J.W. Biomed. Brointon. Mass Spectrom. 19, 655-664, 1990
A; Title: Structural characterization by mass spectrometry of native and recombinant huma A; Reference number: A60982; MUID:91167739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N.Alternate names: preprorelaxin 2
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: A05092; A60982
C;Accession: A05092; A60982
R;Hudson, P.; John, M.; Crawford, R.; Haralambidis, J.; Scanlon, D.; Gorman, J.; Tregear
EMBO J. 3, 2333-2339, 1984
A;Fitte: Relaxin gene expression in human ovaries and the predicted structure of a human
A; Reference number: A05092; MUID:85051298
A; Molecule type: protein
A; Residues: 1,2-19;21-44 <GOW>
A; Residues: 1,2-19;21-44 <GOW>
B; Bullesbach, E.E.; Gowan, L.K.; Schwabe, C.; Steinetz, B.G.; O'Byrne, E.; Callard, I.P.
Bur. J. Biochem. 161, 335-341, 1986
A; Title: Isolation, purification, and the sequence of relaxin from spiny dogfish (Squalu A; Title: Isolation, purification, and the sequence of relaxin from spiny dogfish (Squalu A; Reference number: A91179; MUID:87054035
                                                                                                                                                                                                                                                               A; Contents: annotation; sequence revision
A; Contents: annotation; sequence revision
A; Note: the carboxyl-terminal sequence of chain B was determined to be Arg-Trp
A; Note: the carboxyl-terminal sequence of chain B was determined to be Arg-Trp
C; Reywords: pyroglutamic acid
C; Reywords: pyroglutamic acid
F; 1-14/Domain: chain B (fragments) #status experimental <CHA>
F; 1-14/Domain: chain A #status experimental <CHA>
F; 1-14/Domain: chain B #status experimental conformation of the conformation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MARYMLLLLLAVWVLTGELWPGAEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33 RLCGREFIRAVIFTCGGSRWRRSDILAHEAMGDTFPDADADEDSLAGELDEAMGSSEWLA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.4%; Score 109.5; DB 1; Length 185; 22.7%; Pred. No. 0.0028; tive 22; Mismatches 78; Indels 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 LTKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y Match 15.4%; Score 117; DB 1; Length 44; Local Similarity 24.5%; Pred. No. 0.00013; hes 27; Conservative 6; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QLCGRGFIRALIFACGGSRWATS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 22.79
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-185 <HUD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A60982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: A05092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ă
```

g

g δ

δλ

```
N.Alternate names: Ley I-L
C; Species: Sus scrofa domestica (domestic pig)
C; Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 05-Nov-1999
C; Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 05-Nov-1999
C; Accession: A53024, A49687
R; Burkhardt, E.; Adham, I.M.; Brosig, B.; Gastmann, A.; Mattei, M.G.; Engel, W. Genomics 20, 13-19, 1994
A; Title: Structural organization of the porcine and human genes coding for a Leydig can A; Accession: A53024
A; Accession: A53024
A; Accession: A53024
A; Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-131 cBURN
A; Cross-references: GB:X73636; NID:g871548; PIDN:CAA52016.1; PID:g871549
A; Cross-references: GB:X73636; NID:g871548; PIDN:CAA52016.1; PID:g871549
B; Adham, I.M.; Burkhardt, E.; Benahmed, M.; Engel, W.
Chem. 268, 26668-26672, 1993
A; Title: Cloning of a cDNA for a novel insulin-like peptide of the testicular Leydig
A; Reference number: A49687; MUID:94075362
A; Molecule type: mRNA
A; Residues: 1-131 cADH>
A; Cross-references: GB:X58369
A; Cross-references: GB:X58369
A; Note: sequence extracted from NCBI backbone (NCBIN:140859, NCBIP:140860)
A; Genetics:
A; Genetics:
A; Map position: 19p13.2-p12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                relaxin precursor - rhesus macaque
C; Species: Macaca mulatta (rhesus macaque)
C; Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 12-Jun-1998
C; Accession: A34936
R; Crawford, R.J.; Hammond, V.E.; Roche, P.J.; Johnston, P.D.; Tregear, G.W.
J. Mol. Endocrinol. 3, 169-174, 1989
A; Title: Structure of rhesus monkey relaxin predicted by analysis of the single-copy
A; Fielerence number: A34936; MUID:90073957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.Introns: 64/1
F.1-24/Domain: signal sequence #status predicted <SIG>
F.1-25/Domain: Leydig insulin-like protein chain B #status predicted <BCH>
F.57-105/Domain: connecting C peptide #status predicted <CPEP>
F.106-131/Domain: Leydig insulin-like protein chain A #status predicted <ACH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83 EAMGSSEW-----LALTKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCCKWGC 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 ELL---OWLECOHLFHGLMASGDPMLVLAPOPPDAS-GHHHHRRAAATNPARHCCLSGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 AEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAHEAMGDTFPDADADEDSLAGELD 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.4%; Score 102; DB 2; Length 131;
24.8%; Pred. No. 0.01;
ative 19; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: insulin
F;1-22/Domain: signal sequence #status predicted <SIG>F;23-185/Product: relaxin #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: A34936 A;Status: not compared with conceptual translation A;
                                                Leydig insulin-like protein precursor - pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-131 <BUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 SKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 TRODLLTLC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-185 <CRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                â
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                           Apolecule type: protein
Apolec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 DADA------DEDSLAGELDEAMGSSEWLALTKSPQAFYRGRPSWQ------ 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 PAETMPSSITKDAEILKMMLEFVPNLPQELKATLSER-----OPSLRELQQSASKDSNLN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 -----GTPGVLRGSRDVLAGLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 FEEFKKIILNRQNEAEDKSLLELKNLGLDKHSRKKRLFRMTLSEKCCQVGCIRKDIARLC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 LLAVWYLTGELWPGAEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAHEAMGDTFP 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 LLGVWLLLSQLPREIPGGSTNDFIKACGRELVRLMVEICGSVSWGRTALSLEEPQLETGP 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.0%; Score 106.5; DB 1; Length 182; 21.7%; Pred. No. 0.0053; tive 22; Mismatches 68; Indels 51;
                                  A;Title: Primary structure of the B-chain of porcine relaxin. A;Reference number: A90205; MUID:77157271
Biochem. Biophys. Res. Commun. 75, 503-510, 1977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                    A; Accession: A90205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              엽
```

32; Gaps

13.4%; Score 101.5; DB 2; Length 185; 22.7%; Pred. No. 0.016; tive 22; Mismatches 78; Indels 43; Gaps

Conservative

Query Match Best Local Similarity Matches 42; Conserv

RESULT

δ

```
A; Cross-references: GB:S72482; NID:g632798; PIDN:AAB31371.1; PID:g632799 C; Genetics:
                                                                                            A;Cross-references: GDB:230307; OMIM:146738
A;Map position: 19p13.2-19p12
A;Introns: 64/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein A; Residues: 161-185 <BU2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein
A; Residues: 23-57 <BUE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 SEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 QDLLTLC 129
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Keywords: hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: PC2067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: PN0626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ÓΥ
                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Legiga insulin-like protein precursor - human c; Species: Homo sapiens (man) (5.5 pecies: Homo sapiens (man) (5.5 pecies: Homo sapiens (man) (5.5 pecies: Homo sapiens (man) (5.5 pace: 10.3 May-1994 #sequence_revision 0.3-May-1994 #sequence_revision 0.3-May-1994 #spurkhardt, E.; Adham, I.M.; Brosig, B.; Gastmann, A.; Mattei, M.G.; Engel, W. R; Burkhardt, E.; Adham, I.M.; Brosig, B.; Gastmann, A.; Mattei, M.G.; Engel, W. A; Title: Structural organization of the porcine and human genes coding for a Leydig cell A; Reference number: A53024; MUID:94292172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:X73637
R;Burkhardt, E.; Adham, I.M.; Hobohm, U.; Murphy, D.; Sander, C.; Engel, W.
Hum. Genet. 94, 91-94, 1994
A;Title: A human cDNA coding for the Leydig insulin-like peptide (Ley I-L).
A;Reference number: I54278; MUID:94307715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Raja erinacea (líttle skate)
C;Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 16-Feb-1997
C;Accession: A29543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 LDEAMGSSEWLALTKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCCKWGCSKSEISS 140
                                                                                                                                                                  61 DAPLKPRPAAEIVPSLINQDTETINMMSEEVANLPQELKLTLSERQPALSELQQHVPVLK 120
                                                                                                                                                                                                                    98 ------QAFYRGRPS--WQGTPGVLRG------SRDVLAGLSSSCCKWGCSKSE 137
                                                                                                                                                                                                                                                121 DSNLSFEEFKKIIRKRQSBATDSSPSELRSLGLDTHSRRKRQLYMTLSNKCCHIGCTKKS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 PGAEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAHEAMGDTFPDADADEDSLAGE 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 PNWEERS-----RLCGRDLIRAFIYLCGGTRWTRLPNFGNYPI------39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 MEEKM-----GFAKKCCAIGCSTEDFRM 62
                                                              1 MARYMLLLLLAVWVLTGELWPGAEARAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Bullesbach, E.E.; Schwabe, C.; Callard, I.P.
Biochem. Biophys. Res. Commun. 143, 273-280, 1987
A;Title: Relaxin from an oviparous species, the skate (Raja erinacea).
A;Reference number: A29543; WUID:87156758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.2%; Score 100.5; DB 2; Length 64; 22.1%; Pred. No. 0.0071; Live 11; Mismatches 25; Indels 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; not compared with conceptual translation A;Molecule type: DNA
A;Residues: 1-131 <BUR>
                                                                                                                             61 EAMGDTFPDADADEDSLAGELDEAMGSSEWLA-----LTKSP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        relaxin - little skate (fragments)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 22.18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: ovary C; Superfamily: insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein A; Residues: 1-64 <BUL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: B53024
                                                                                                                                                                                                                                                                                                                        138 ISSLC 142
                                                                                                                                                                                                                                                                                                                                                                        181 LAKFC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 LC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :1
63 VC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qγ
                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                       qq
                                                                                                                                         ŏ
                                                                                                                                                                                                                                 ò
```

```
R;Buellesbach, E.E.; Schwabe, C.
Blochem. Blophys. Res. Commun. 196, 311-319, 1993
A;Title: Mouse relaxin: synthesis and biological activity of the first relaxin with a
A;Reference number: PN0626; MUID:94030011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Note: proteins with and without 184-Tyr were synthesized, their biological activiti C;Superfamily: insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 16-Jul-1999
C; Dates: 07-May-1995 #sequence_revision 21-Jul-1995
C; Accession: S48082; PC2067; PN0626
C; Accession: S48082; Powler, K.J.; Summers, R.J.; Cronk, M.; Shine, J.; Tregear, J. Mol. Endocrinol. 10, 15-23, 1993
A; Title: The mouse relaxin gene: nucleotide sequence and expression.
A; Reference number: S48082; MUID:93199663
A; Status: preliminary
A; Status: preliminary
A; Mullinary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 RLALSQEEPALLARQATEVVPSFINKDAEPFDTTLKCLPNLSFELKAVLSEAQASLPELQ 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-185 <EVA>
A; Cross-references: EMBL: 227088; NID: 9414780; PIDN: CAA81611.1; PID: 9414781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 R-----EDSLAHEA--MGDTFPDADAD-------EDSLAGELDEAMGSSEWLA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67; Indels 56; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MARYMLLLLLAVWVL-----TGELWPGAEARAAPYGVRLCGREFIRAVIFTCGGSRW 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSSRFLIQLLGFWLLLSQPCRTRVSEEWMDG-----FIRMCGREYARELIKICGASVG 53
                                                                                                                                                                                                                                                                                                89 EWLA------LITKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCCKWGCSK 135
                                                                                                                                                                                                                                                                                                                                                                   68 OWLERRHLLHGLVADSNLTLGP-----GLOPLPQTSHHHRHHRAAATNPARYCCLSGCTO 122
                                                                               37; Indels 46; Gaps
                                                                                                                                              33 RLCGREFIRAVIFTCGGSRW----RRSDILAHEAMGDTFPDADADEDSLAGELDEAMGSS 88
                                                                                                                                                                                                                         Query Match
13.0%; Score 99; DB 2; Length 185;
Best Local Similarity 24.7%; Pred. No. 0.029;
Matches 47; Conservative 20; Mismatches 67; Indels
Query Match
Best Local Similarity 25.2%; Pred. No. 0.02;
Matches 32; Conservative 12; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;23-57,161-185/Product: relaxin #status experimental cmal/
F;23-57/Domain: chain B #status experimental cCHB>
F;161-185/Domain: chain A #status experimental cCHA>
F;161-185/Domain: chain A #status experimental cxRa>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ,161-185/Product: relaxin #status experimental <MAT>
```

_	C;Date: 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 24-Sep-1999 C:Accession: A01614
OW 122 CARRESTOR 123 CARRESTOR 173	R; Hudson, P.; Haley, J.; Cronk, M.; Shine, J.; Niall, H.
	Nature 291, 127-131, 1981 A:Title: Molecular Cloning and characteristics of accountable
Db 174 GCSRRSIAKL 183	A: Reference number: A01614; MUID: 81197624 A: Accession: A01614
RESULT 11	A; Molecule type: mrnA A Besidnes 1106 / rms
A44559 relaxin 1 precursor - human	A:Cross-reference GB:J00780; GB:M25468; NID:9206606; PIDN:AAA42029.1; PID:9206607 C:Superfamily: inclided the control of the c
	C. Corporation 19 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
C:Date: 03-Feb-1994 #sequence_revision 07-Oct-1994 #text_change 18-Jun-1999 C:Accession: B05092: A44556	7.7 Z2/Commin: Signal Sequence #Status predicted <sig> F:23-57/Domain: Status predicted <rxb> F:73-57 162-166 for call B #Status predicted <rxb></rxb></rxb></sig>
R; Hudson, P.; John, M.; Crawford, R.; Haralambidis, J.; Scanlon, D.; Gorman, J.; Treapen	F.58-162/Domain: relaxin connecting C peptide #status predicted <pre>F.162.10c</pre>
redicted structure	F.36-173.48-186.772-177/Disulfide bonds: #status predicted <rxa> F.36-173.48-186.772-177/Disulfide bonds: #status predicted F.163/Modified site: nvrnolidams canamaria in the status predicted</rxa>
A; Accession: B05092	First conditions calboxyild dold (Gin) (in mature form) #status predi
A. Nes. Luds (HII)> A. Cross. references: GB:X00949; NID:935932; PIDN:CAA25461.1; PID:935933	atch 12.9%; Score 98; DB 1, cal Similarity 23.8%; Pred. No. 0.036;
Nimeson, F.; Harey, J.; John, M.; Cronk, M.; Crawford, R.; Haralambidis, J.; Tregear, G. N. Haralambidis, J. Haralambidis, J.; Tregear, G. N. Haralambidis, J.; Tregear, G. N. Haralambidis, J. Haralambidis,	матспе
A) ILLE: Structure of a genomic clone encoding biologically active human relaxin. A) Reference number: A44559; MUID:83141755	
A; Modecule type: DNA	MSSRLLLQLLGFWLFLSQPCRARVSEEWMDQV
A) residues: 1185 <bu2> C) Cross-references: GB: X00949; NID:935932; PIDN:CAA25461.1: PID: 335933</bu2>	54
disulfide bonds.	
C;Genetics: A;Gene: GDB:RLN1	OY 87SSEWLALTKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCCKWGC 133
A;Cross-references: GDB:119552; OWIM:179730 A;Map position: 9pter-9q12	Db 118 PALSDSVVSLEGFKKTFHNQLGEAEDGGPPELKYLGSDAQSRKKRQSGALLSEQCCHIGC 177
C; Superfamily: insulin C; Keywords: hormone.	Qy 134 SKSEISSLC 142
F.1-25/Domain: signal sequence #status predicted <sig></sig>	Db 178 TRRSIAKLC 186
F;26-77,160maln: relaxin 1 chain B #status predicted <bch> F;26-77,162-185/Product: relaxin 1 #status predicted <mat></mat></bch>	
F/30 136/JOMMAIN: relaxin 1 connecting C peptide #status predicted <cpep> F/36-185/JOMMAIN: relaxin 1 chain A #status predicted <aah></aah></cpep>	
r;35-1/2,47-185,171-176/Disulfide bonds: #status predicted	relaxin 1 precursor - chimpanzee (fragment) C;Species: Pan troglodytes (chimpanzee)
Query Match 13.0%; Score 98.5; DB 1: Length 185.	C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999 C;Accession: S42783
23.8%; Pred. No. 0.032; ative 19; Mismatches 79;	R; Evans, B.B. submitted to the EMBL Data Library, November 1993
5 G	A; Reference number: S42776 A; Accession: S42783
Db 1 MPRLFLEFELLLENGFSRAVAAKWKDDVIKLCGRELVRAQIAICGMSTWSKRÈLSOF 60	A Molecule type: mrna A Residues: 1-166 <eva></eva>
	A/cross references: EMBL:227225; NID:g415996; PIDN:CAA81739.1; PID:g415997 C.Genetics:
II VPALK 1	A; Gene: rlx1 C; Superfamily: insulin
	Fil-5/Domain: signal sequence (fragment) #status predicted <sig></sig>
Db 121 DSNLSFEEFKKLIRNRQSEAADSNPSELKYLGLDTHSQKRRRPYVALFEKCCLIGCTKRS 180	. o rovriounce: relaxin 1 #status predicted <mat></mat>
Qy 138 ISSLC 142	Query Match 12.6%; Score 95.5; DB 2; Length 166;
Db 181 LAKYC 185	LOCAL SIMILATILY 23.1%; Pred. No. 0.056; les 36; Conservative 18; Mismatches 55;
RESULT 12	
RXRT relaxin precursor - rat	
	QY 76 -SLAGELDEAMGSSEWLALTKSPQAFYRGRPS 106

Ø

Gaps

20;

```
A; Molecule type: protein
A; Molecule type: protein
A; Mosious 67-116 < HLE>
A; Residues: 67-116 < HLE>
A; Residues: 67-116 < HLE>
A; Hetru, C.; Li, K.W.; Bulet, P.; Lagueux, M.; Hoffmann, J.A.
Buchem. 201, 495-499, 1991

A; Hetru, C.; Li, K.W.; Bulet, P.; Lagueux, M.; Hoffmann, J.A.
A; Holecule type: Isolation and structural characterization of an insulin-related molecule, A; Reference number: S17851; MUID: 92037603
A; Reference number: S17851; MUID: 92037603
A; Molecule type: protein
A; Molecule type: protein chain B #status experimental < ACH>
F; 34-64/Product: insulin-related protein chain A #status experimental < ACH>
F; 123-143/Product: insulin-related protein chain A #status experimental < ACH>
F; 123-143/Product: insulin-related protein chain A #status experimental < ACH>
F; 123-143/Product: insulin-related protein chain A #status experimental < ACH>
F; 123-143/Product: insulin-related protein chain A #status experimental < ACH>
F; 123-143/Product: Insulin-related protein chain A #status experimental < ACH>
F; 123-143/Product: Insulin-related protein chain A #status experimental < ACH>
F; 123-143/Product: Insulin-related protein chain A #status experimental < ACH>
F; 123-143/Product: Insulin-related protein chain A #status experimental < ACH>
F; 123-143/Product: Insulin-related protein chain A #status experimental < ACH>
F; 123-143/Product: Insulin-related protein chain A #status experimental < ACH>
F; 123-143/Product: Insulin-related Protein Chain A #status A #stat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 AHEAMGDTFPDADADEDSLAGELDEAMGSSEWLALTKSPQAFYRGRPSWQGTPGVLRGS- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 FKKASQDV-SDSESEDNYWSGQSADEAAEAAAALPPYP---ILARPS---AGGLLTGAV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 LILLLAVWVLT----GELWPGAEARA-APYGV-RLCGREFIRAVIFTCGGSRWRRSDIL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.6%; Score 88; DB 2; Length 145; 26.7%; Pred. No. 0.26; tive 28; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: June 27, 2002, 16:09:27
A; Reference number: S07773; MUID:90126826
A; Accession: S07773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 -RDVLAGLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 FRRRTRGVFDECCRKSCSISELQTYC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 26.77
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Job time: 211 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL: Z29963
R;Laqueux, M.; Lwoff, L.; Meister, M.; Goltzene, F.; Hoffmann, J.A.
R;Laqueux, M.; Lwoff, L.; Meister, M.; Goltzene, F.; Hoffmann, J.A.
Bur. J. Biochem. 187, 249-254, 1990
A;Title: cDNAs from neurosecretory cells of brains of Locusta migratoria (Insecta, Orthd A;Reference number: S07774; MUID: 90126827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Kromer-Metzger, E.; Lagueux, M.
Eur. J. Biochem. 221, 427-434, 1994
A;Title: Expression of the gene encoding an insulin-related peptide in Locusta (Insecta, A;Reference number: 843224; MUID:94222089
A;Accession: 843224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A)tCross.references: EMBL:X17024. NID:99529; PID:99530 R; Hoffmann, J.; Luu, B. R; Hietter, H.; van Dorsselaer, A.; Green, B.; Denoroy, L.; Hoffmann, J.; Luu, B. Eur. J. Blochem. 187, 241-247, 1990 A; Title: Isolation and structure elucidation of a novel 5-kDa peptide from neurohaemal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Locusta migratoria (migratory locust)
C;Date: 28-Sep-1994 #sequence_revision 12-Apr-1996 #text_change 12-Jun-1998
C;Accession: S43224; S07774; S07773; S17851; S42153
                                                                                                                                                                                                                                                                                                                                                                                         relaxin - dog (fragments)
C;Species: Canis lupus familiaris (dog)
C;Date: 27-Sep-1994 #sequence_revision 26-May-1995 #text_change 26-May-1995
C;Accession: B538P9; A53F9; A53F9; R5;Evart, D.R.; Henzel, W.J.; Vandlen, R.
J; Protein Chem. 11, 247-253, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 VRLCGREFIRAVIFTCGGSRWRRSDILAHEAMGDTFPDADADEDSLAGELDEAMGSSEWL 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 LKACGRDYVRLQIEVCGSSWWGRK------35
                             73 ANLPPELKAAL--SERQPSLPEPQQYVPALKDSNLSFEEFKKLIRNRQSEAADSNPSELK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: Purification and sequence determination of canine relaxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92 ALTKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----DNYIKMSDKCCNVGCTRRELASRC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.8%; Score 89.5; DB 2; Length 59; 20.7%; Pred. No. 0.075; tive 11; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: placenta A; Note: sequence extracted from NCBI backbone (NCBIP:115401) A; Accession: A53879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Note: sequence extracted from NCBI backbone (NCBIP:115399) C;Superfamily: insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1-35,36-59/Product: relaxin #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F.1-35/Domain: chain B #status experimental <CHB> F.36-59/Domain: chain A #status experimental <CHA> F:96-621-59,45-50/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   insulin-related protein precursor - migratory locust
                                                                                                                                                                     107 WQGTPGVLRGSRDVLAGLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 20.7%; Pred. No. 20.7%; Matches 23; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: A53879; MUID: 93000391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-131, 'T', 133-145 <LAG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein
A; Residues: 1-35 <STE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein A; Residues: 36-59 <ST2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-145 <KRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: S07774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: B53879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36 ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Keywords:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
                                                                                                                                                                                                                                                                                                                                      14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δy
                                                                                                                                       δ
```

			•

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

June 27, 2002, 16:08:11; Search time 58.57 Seconds (without alignments) 419.417 Million cell updates/sec Run on:

US-09-781-077-2 Title: Perfect score: Sequence:

1 MARYMILLILAVWVLTGELW......GLSSSCCKWGCSKSEISSLC 142

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

562222 Total number of hits satisfying chosen parameters:

562222 seqs, 172994929 residues

Searched:

Minimum DB seg length: 0 Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

sp_vertebrate:*
sp_unclassified:* sp_human:* sp_invertebrate:* sp_mammal:*
sp_mhc:*
sp_organelle:*
sp_phage:* SP_rvirus:*
SP_bacteriap:* 1: sp_archea:* 2: sp_bacteria:* sp_plant:*
sp_rodent:*
sp_virus:* sp_archeap:* SPTREMBL_19:* sp_fung1:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	O9depB rana escule O9mykB felis silve O9n0t9 camelus dro O99k47 galago cras O9n0t8 dama dama (O9n0zB capra hircu O9k46 galago cras O9hwy2 pseudomonas O9hwy2 pseudomonas O9ndz2 leishmania O57687 taenopygia P79890 gallus gall O9fia4 arabidopsis O9fis9 arabidopsis O9kxri streptomyce O554959 streptomyce O554959 agrius conv
SUMMARIES	ID	Q9DEP8 Q9MYR8 Q9M0T9 Q9M0Z8 Q9M0Z8 Q9M0Z2 Q9MW22 Q9MW22 Q9FEA4 Q9FE95 Q9FEA4 Q9FE95 Q9KZR1 Q64959
	Query Match Length DB	20.1 155 113.7 180 6 5 113.7 180 6 6 113.6 113.6 112.9 131 6 111.6 181 6 110.7 172.2 5 10.5 187 13 10.5 142.9 10.3 454.2 10.2 10.3 2591 2 10.2
о́Р	Score Ma	152.5 104 103.5 101 101 101 101 101 101 101 10
	Result No.	1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2

085020 mycobacteri 087313 mycobacteri 0922x3 mus musculu 09hxj7 pseudomonas	Q9cqv4 mus musculu Q9uph6 homo sapien	Q9la28 shigella dy O9rtdl deinococcii	٠,	052599 agrobacteri	O33849 mycobacteri O06075 mycobacteri	O9w4m6 drosophila	098ta7 osteoglossu	095082 homo sapien	Ogfor for sapien	C210d/ Streptomyce	Observed of the gor	D72046 missbart	Ogaqya amyoolateri	094006 Orwan satis	083380 rat loubout	Ogan 1 Comment	Obrew Colcyla Cep	Oct to beendomonas	Usigeo oryza sativ	091tc2 arabidopsis	U6/939 hepatitis b	Volyso neparitis b
085020 087313 0922X3 09HXJ7	Q9UPH6 Q9UPH6	Q9RTD1	Q9S0R7	053649	006075	OSW4M6	095082	09P0V3	Q9F0D7	028431	092XB0	P72045	Q939Y9	Q94E06	083380	Q9GPL1	092FX3	09160	COLITION	067939	067938	
2 11 16	4 6	16	~ ~	16	16	۰ ۲	4	4	7			16		10		S	7	10	10	12	12	
2129 2569 344 380	513	319	6239 258	663	667	111	479	963	1505	33	653	999	1858	477	614	173	174	299	1067	281	400	
100.1	10.0	0.0	თ თ თ თ	6.6	6.0	, o	9.7	6.7	7.6	9.6	9.6	9.6	9.6	ي د .	υ. υ.	ر ت	9.5	9.5	9.5	9.4	9.4	
77 76.5 76.5 76.5	76	ι. L	75	7.5	75	74.5	74	74	73.5	73	73	73	73	 	0.7	7/	7.5	72	72	71.5	71.5	
17 18 19 20 21	22	24	72 72	27	7 7 8 7 8 7 8	30	31	32	33	4.0	32	9 1	7 0	0 0	n c) r	4 T	7.7	43	44	45	

ALIGNMENTS

RESULT 1 09DEP8 1D 09DEP8, AC 09DEP8, DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) GN 1NGT2	 SEQUENCE FROM N.A. TISSUE=TESTIS; MEDLINE=21009007; p MEDLINE=21009007; p De Rienzo G., Aniel "Isolation and char. relaxin/insulin fam Frdaxin/insulin fam Frdaxin/insulin fam Frdaxin/insulin fam Frdaxin/insulin fam Frdaxin/insulin fam Frdocrinology 142:3 -1 - SIMITARITY: BELG EMBL; AJ298874; CAC. INTERPRO; IPR00075; Frdam; PF00049; InsulinerPro; IPR00049; InsulinerPro; ROMO49; INSU SWART; SMO009; INSU	SQ SEQUENCE 155 AA; 17470 MW; 517ADA5385026E34 CRC64; Query Match 20.1%; Score 152.5; DB 13; Length 155; Best Local Similarity 27.7%; Pred. No. 8e-08; Matches 49; Conservative 21; Mismatches 40; Indels 67; Gaps Qy 4 YMLLLLAWWLTGELW-PGAEARAAPYGVRLGREFIRAVIFTCGGSRWRR 54 : :

```
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 LAHEAMGDTFPDADADEDSLAGELDEAMGSSEWL-----ALTKSPQAFYRGRPSWQ 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 QHREPRQAPAALPEIVSSSITSGABALNGMLEYIPDLPQELKATLSEREPSFRELQPSLK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 DSNLNLEEVEKSILGRONEAEDQSLSQLGRSRLDAHSRIKRSDYIRYSDRCCNVGCTRKE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MARYMLLLLLAVWVLTGELWPGAEARAAPYG----VRLCGREFIRAVIFTCGGSRWRRSDI 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MLRLFLSHLLGVWLLL----SLRARKIPAQEEVLKACGREFVRLQIRICGSLSWGKSSQ 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48; Gaps
                          61 RSNPNRDFLDWLNRASLEDPDRLNSLYAESHMAPNPPFSSLQKDDPTWEQLHGALYDPLV 120
----SDIL-----DSLAGELDEAMG 86
                                                                                                                                                                                                                                                                                                                                    MEDIINE-99115216. PubMed-9915995;
Klonisch T., Hombach-Klonisch S., Froehlich C., Kauffold J.,
Steger K., Huppertz B., Fischer B.;
"Nucleic acid sequence of feline preprorelaxin and its localization
                                                        87 SSEWLALTKSPQAFYRGRPSWQGTPGV-LRGSRDVLAGLSSSCCKWGCSKSEISSLC 142
                                                                       121 TEE------QOGVGLRMKRS--AGPALSCCQRGCTKNELMKFC 155
                                                                                                                                                                                                                                                 Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.7%; Score 104; DB 6; Length 180; 22.2%; Pred. No. 0.0076; rtive 21; Mismatches 75; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPK000739; Insulin_IGF_relaxin.
SMART; SM00078; I1GF; 1.
PROSITE; PS00262; INSULIN; 1.
SEQUENCE 180 AA; 20360 MW; 4C2CF371C698AF9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                         01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                 within the feline placenta.";
Biol. Reprod. 60:305-311(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138 ISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176 LADLC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PREPRORELAXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09N0T9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               610N60
                                                                                                                                                                                                                                             RELAXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    m
                                                                                                                                                                     Q9MYK8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                          7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
Q9N0T9
                                                                                                                                            RESULT
                                                                                                                                                        Q9MYK8
                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
              ŏ
                                      g
                                                                    ŏ
```

```
Klonisch T., Froehlich C., Tetens F., Fischer B., Hombach-Klonisch S., Molecular remodeling of members of the relaxin family during primate evolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Galago crassicaudatus (Thick-tailed galago) (Otolemur crassicaudatus). Butacoa; Chordata, Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Strepsirhini; Galagonidae; Otolemur.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45; Indels 60; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 ERQPSAEPQQPALKDSNLNFEEFKKIIFDRQNBEEDESLSELKNLGLDKHSEK----- 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 PRPAPKPALRPALSQDKKPRLRSGPPAEIMPSSITKDAETLTTMLEFTPNLPQELTATLS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 DIFPDADADEDSLAG-------ELDEAMGSSEWLALTKSPQAFYRGRPS 106
                                                                                                                                                                                                                                                                                                                                                                                                         55 -----AMG 64
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                       1 MARYMILLILAVWVLTGELWPGAEARAAPYGVRLCGREFIRAVIFTCGGSRWRR----- 54
Camelus dromedarius (Dromedary) (Arabian camel).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; CetarLiodactyla; Tylopoda; Camelidae; Camelus.
NCBI_TaxID=9838;
                                                                                                                                                                                                                                                                                                                                                             91;
                                                                                           13.6%; Score 103.5; DB 6; Length 199; 18.1%; Pred. No. 0.0096; Live 24; Mismatches 62; Indels 91.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 13.3%; Score 101; DB 6; Length 131; Best Local Similarity 24.5%; Pred. No. 0.01; Marches 39; Conservative 15; Mismatches 45; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOJ. BYOLLEY.

MOJ. BYOLL EVOL. 0:0-0(2001).

-i- SUBCELDULAR LOCATION: SECRETED (BY SIMILARITY).

-i- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.

EMBL; AF317624, AAG42317.1; -

InterPro; IPR000739; Insulin_IGF_relaxin.

PROSTITE; PS000262: INSULIN; 1.

SEQUENCE 131 AA; 14414 MW; F18AFA9ACFC85943 CRC64;
                                                                                                                                                                                                                        HSSP; P01348; IRLX.
InterPro; IPR000739; Insulin_IGF_relaxin.
SMART; SM0078; IIGF; IIS IIGE IIS PROSTIE; SS00262; IISULIN: 1.
SPROSTIE; PS00262; INSULIN: 1.
SEQUENCE 199 AA; 22386 MW; F69BBD7E4F4A8089 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 WQGTPGVLRGSRDVLAGLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RELAXIN-LIKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 39; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9463;
                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9GK47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           염
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                      ŏ
```

4;

```
PROFEDAXIN.
Galago crassicaudatus (Thick-tailed galago) (Otolemur crassicaudatus).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Primates; Strepsirhini; Galagonidae; Otolemur.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE-EMBRYONIC TROPHOBLAST, PLACENTA;
Klonisch T., Froehlich C., Tetens F., Fischer B., Hombach-Klonisch S.;
"Molecular remodeling of members of the relaxin family during primate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 EAMGSSEWIALTKSPQAFYRGRPSWQGTPGVLR--GSRDVLAGLSSS------ 127
                                                                                                                                                                                                                                                                                                                                                                                                                                  23 AEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAHEAMGDTFPDADADEDSLAGELD 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 ----SE------SGRPVAGGDRELLEWLEGOHLLHGLMASGDPVLVLAPQPLP 95
                                                        Hombach-Klonisch S., Tetens F., Kauffold J., Steger K., Fischer B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score ov, --
Pred. No. 0.52;
"" " " " " " " " " " " " " " " " Gaps
                                                                          Klonisch T.; "Molecular cloning and localization of caprine relaxin-like factor (RLF) mRNA within the goat testis."; Mol. Reprod. Dev. 53:135-141(1999).
                                                                                                                                                                                                                                                                                                                                                                                                             82;
                                                                                                                                                                  Query Match
11.6%; Score 88; DB 6; Length 131;
Best Local Similarity 21.4%; Pred. No. 0.22;
Matches 33; Conservative 14; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOI. BIOI. EVOI. 0:0-0(2001).
-!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
EMBL; AF317625; AAG42318.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.3%; Score 86; DB 6; Length 188; 21.3%; Pred. No. 0.52; tive 21; Mismatches 64; Indels
                                                                                                                                                                                                                                                          Interpro; IPR000739; Insulin_iGF_relaxin.
Pfan, PF00049; Insulin; 1.
PROSTIE; S800202; INSULIN; 1.
PROSTIE; P$00202; INSULIN; 1.
SEQUENCE 131 AA; 14160 MW; 2A82EB59EA07313A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P04000; 6RLX.
InterPro; IPR000739; Insulin_IGF_relaxin.
SMART; SM00078; ILGF; I.
PROSITE; P800262; INSULIN; I.
SEQUENCE 188 AA; 21573 MW; 77551629B82B9A66 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oggk46;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96 QASRHHHRRATAINPARHCCLSGCTRQDLLTLC 129
                             TISSUE=TESTIS;
MEDLINE=99260294; PubMed=10331451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 21.3%
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
              SEQUENCE FROM N.A.
                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9GK46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9GK46
δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
```

œ

5,

```
187 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1998 (TrEMBLrel. 06, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000209; Peptidase_S8.
Pfam; PF00082; Peptidase_S8; 2.
PRINTS; PR00723; SUBTILISIN.
PROSITE; PS00138; SUBTILASE_SER; 1.
                                                                                                                                                                                                                                                                                                                        MEDLINE=98146435; PubMed=9477341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 06, (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
POSSIBLE SERINE PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1601 DETRFORDYAA 1611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 GVLRGSRDVLA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Taenopygia guttata.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GF-II PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=72052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEROPS; SOB.UPW;
                                                                                         NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                         STRAIN-FRIEDLIN;
                                                                                                                                                                 STRAIN-FRIEDLIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-EMBRYO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=EMBRYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Taenopydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      057687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
057687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
    4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-ATC. 15692 / PAO1;
MEDLINE=20437337, PubMed=10984043;
MEDLINE=20437337, PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Goltry L., Tolentino E., Westbrock-Waddman S., Yuan Y.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
Opportunistic pathogen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 TFPDADADEDSLAGELDEAMGSSEW--LALIKSPQAFYRGRPSWQGTPGV---LRGSRDV 120
                                                                                                                       52 WRRSDILAH-----EAMGDTFPDADADEDSLAGELDEAMGSSEWLALTKSPQAFYRG 103
                                                                                                                                                  | : | : | : | : :| : | : :| : : | : :| : : | : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| :
                                                                                                                                                                                                                                                               107 EMNLPSPELQQYPPTLKGSDISFEEVKNNIHNEQGEAEDNSHSELQNLGLDTHSRKKRER 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 LLLLLAVWVLTGELWPGAEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAHEAMGD 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 LIPLILVEFFLGELOPLPHGLAMPLFIAALLSMFVNLPLF----GAYKRGLIATQKA--- 74
                                                         1 MARYMLLLLLAVWVLTGELWPGAEARA-APYGVRL-----CGREFIRAVIFTCG--GSR 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 10.9%; Score 82.5; DB 16; Length 139; Best Local Similarity 26.0%; Pred. No. 0.83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE004821; AAG07433.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 139 AA; 15161 MW; 9F5D69D2981A389A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1722 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                 121 LAGLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                              167 YMSPLOKCCRIGCTKRSLARFC 188
                                                                                                                                                                                                                       104 R-----PSWOGTPGVLRGS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2000 (TrEMBLRel. 15, 01-0CT-2000 (TrEMBLRel. 15, 01-DEC-2001 (TrEMBLRel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL PROTEIN PA4046.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 LAGLSSSCCKW 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 LLGVTSLVLFW 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9NDZ2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09HWY2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9NDZ2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09HWY2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                      æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09NDZ2
                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              09HWY2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                        g
                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                      ŏ
                                                                                                                              ŏ
                                                                                                                                                                                                                       Óγ
```

```
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Passeriformes; Passeroidea; Passeridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1507 LLLWLHTGNLHRWWDSAQLQ--------CEARRWARA---RHRSTADT 1543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 FPDADA-DEDSLAGELDEAMGSSE------WLALTKSPQAFYRGRPSW--QGTP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40; Indels 44; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 LAVWVLTGEL---WPGAEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAHEAMGDT 66
Leishmania major.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97426547; PubMed=9278533;
Holzenberger M., Jarvis E.D., Chang C., Grossman M., Nottebohm F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scharff C;;
%Selective expression of insulin-like growth factor II in the song
bird brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oliver K., Harris D., Ivens A.C., Quail M., Rajandream M.A., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M., Smith D.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 10.7%; Score 81; DB 5; Length 1722; Best Local Similarity 24.4%; Pred. No. 23; Matches 32; Conservative 15; Mismatches 40; Indels Matches 32; Conservative 15; Mismatches 40; Indels 40; Mismatches 40; Indels 40; Mismatches 40; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "A physical map of the Leishmania major Friedlin genome.";
Genome Res. 8:135-145(1998).
EMBL, AL356713; CAB92392.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Holzenberger M.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 1722 AA; 182741 MW; 8148DD78AC52DD1F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
```

```
4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Darling D.C., Brickell P.M.;
Nucleotide sequence and genomic structure of the chicken insulin-like
growth factor-II (IGF-II) coding region.";
Gen. Comp. Endocrinol. 102:383-287(1996).";
-I-SUBCELLUIAR LOCATION: SECRETED (BY SIMILARITY).
EMBL: 882962; AAB46818.1;
EMBL: 882966; AAB46818.1;
-HSSP: P01344; IGF2.
                                                                                                                                                                                                                                                                                                                                                                                                   60 HEAMGDTFPDADADEDSLAGELDEAMGSSEWLALTKSPQAFYRGRPSWQGTPGVLRGSRD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1997 (TEMBLE-1. 03, Last Sequence update)
01-DEC-2001 (TEMBLE-1. 03, Last Sequence update)
PREPRO-INSULIN-LIKE GROWTH FACTOR-II.
Gallus gallus (Chicken).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                        2 ARYMLLLLLAVWVLTGELWPGAEARAAPYGV--RLCGREFIRAVIFTCGGSRWRRSDILA 59
                                                                                                                                                                                                                                                                                                                                                               46 -------GRINNRR 61
                                                                                                                                                                                                                                                                                                                            64;
L J. Neurosci. 17:6974-6987(1997).

- SUBCELLUIAR LOCATION: SECRETED (BY SIMILARITY).

R EMBL, AJ23165; CAAll145.1;

R HSRS; PO1344; 1GF2.

R PREME, PRO0049; Insulin, IGF_relaxin.

R PRINTS; PRO00276; INSULIN;

R PRINTS; PRO00276; INSULIN.

R PRINTS; PRO00276; INSULIN.

R PRINTS; PRO00276; INSULIN.

R PRINTS; PRO00277; INSULIN.

R PRINTS; PRO0078; INSULIN.

R PRINTS; SMON1048; INSULIN.

SMART; SMON1048; INSULIN.

B DEACTHER: SMON1078; IIGF_INSULIN.

B DEACTHER: MONO1078; IIGF_INSULIN.
                                                                                                                                                                                                                                                                                 10.5%; Score 80; DB 13; Length 187; 23.1%; Pred. No. 2.1; tive 8; Mismatches 38; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
10.5%; Score 80; DB 13; Length 187;
Best Local Similarity 22.4%; Pred. No. 2.1;
Matches 32; Conservative 10; Mismatches 37; Indels
                                                                                                                                                                                                                CHAIN 24 187 IGF-II PRECURSOR.
SEQUENCE 187 AA; 20908 MW; 3C7EADA8F7D2CE8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20837 MW; B301581CD4878EEC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0276; INSULINA.
PRINTS; PR00277; INSULINB.
ProDom; PD001048; Insulin_IGF_relaxin; 1.
SMART; SM00078; IIGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000739; Insulin_IGF_relaxin.
Pfam; PF00049; Insulin; 1.
                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1997 (TrEMBLrel. 03, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-96397665; PubMed-8804558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 VLAGLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 FNRGIVEECCFRSCDLALLETYC 84
                                                                                                                                                   SMART; SM00078; IIGF; 1.
PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 23.1%
Warches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9031;
                                                                                                                                                                                      Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P79890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
P79890
 ô
                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                               οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
```

```
8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Structural analysis of Arabidopsis thaliana chromosome 5. V. Sequence features of the regions of 1,381,565 bp covered by twenty one physically assigned Pl and TAC clones.", DNA Res. 5.131-145(1998).
BMBL, AB010693; BAB10876.1, InterPro; IPR001584; Rvc.
InterPro; IPR001584; Rvc.
Ffam; PF00065; rvc; l.
SMART; SM00343; Zh-CZHC; l.
                                                        60 HEAMGDTFPDADADEDSLAGELDEAMGSSEWLALTKSPQAFYRGRPSWQGTPGVLRGSRD 119
                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
NCBI_TaxID=3702;
2 ARYMLLLLLAVWVLTGELWPGAEARAAPYGV--RLCGREFIRAVIFTCGGSRWRRSDILA 59
                    1151 GIEATRISRGLHLMQRKYI-----TDLLKKHNMLDTKPVSTPMSPTPKLSL 1196
                                                                                     46 ------VGRNNRR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98344145; PubMed-9679202;
Kaneko T., Kotani H., Nakamura Y., Sato S., Asamizu E., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 LAG-ELDEA-----MGSSEWLALTKSPQAF-----YRGRPS---WQGTPGVLRGSRD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 GAEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAHEAMGDTFPDADADEDS----- 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 26.0%; Pred. No. 23;
Matches 39; Conservative 16; Mismatches 39; Indels 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1429 AA; 159492 MW; 7B20CCFB1A9BC263 CRC64;
                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) POLYPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OFFE95;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
SIMILARITY TO UNKNOWN PROTEIN.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                             PRT; 1429 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 542 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1253 YLAGTKSHGIFLRSDTPLTIHAFSDADWGC 1282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 VLAGLSS-----SCCKWGC 133
                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
                                                                                                                 120 VLAGLSSSCCKWGCSKSEISSLC 142
                                                                                                                                              62 INRGIVEECCFRSCDLALLETYC 84
                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-COLUMBIA;
                                                                                                                                                                                                                      O9FLA4
                                                                                                                                                                                            12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9FF95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
                                                                                                                                                                                       RESULT
Q9FLA4
ŏ
                          q
                                                        á
                                                                                   g
                                                                                                                 ŏ
                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DT
DT
DE
OS
```

4;

Gaps

64;

```
054959
                                                                                                                                                                             15
                            Matches
                                                                                                                                                                             RESULT
                                                                                                                                                                                          054959
                                                                                                                                                                                                                     δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δy
                                                                               Ω
                                                                                                             ð
                                                                                                                                                                                                                                                                              7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.,
"A set of ordered cosmids and a detailed genetic and physical map for
                                                                                                                                                                                                                                                                                                                                                                             262 FWGWAEVNIKPWESLLKELREGNERTKW--INREPYAY-----WKGNPWYAETRQDLMK 313
                                                                                                                                                                                                                                                                                                                                                            70 ----ADAD---EDSLAGELDEAMGSSEWLALTKSPQAFYRGRPSWQGTPGVLRGSRDVLA 122
                                                                                                                                                                                                                                                                                                                                   -----ETLDIVFPDWS 261
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                      20 WP-----GAEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAHEAMGDTFPD-- 69
                                                                                                               Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M., Miyajima N., Tabata S., Sequeni "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequeni features of the 1.6 Mb regions covered by twenty physically assigned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                 62;
                                                                                                                                                                                                                                                  10.4%; Score 79; DB 10; Length 542; 21.9%; Pred. No. 9.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                              19; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brown S.P., Harris D.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
EMBL; AL353832; CAB88833.1; InterPro; IPROU1087; Lipase_GbSL.
Pfam; PF00657; Lipase_GBSL, 1.
SEQUENCE 454 AA; 47507 MW; 9F36FAACF4D8E45D CRC64;
                                                                                                                                                                                                     EMBL: AB005244; BAB10058.1; -. SE3C11327A77F26D CRC64; SEQUENCE 542 AA; 62587 MW; 583C11327A77F26D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                                                                    224 WPVVRATEFAGANAPSPPPLFRYCGNE-------
                                                                                                                                                                                                                                                                                                                                                                                                                     123 GLSSSCCKW-----GCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                      | :| :| | :| | 314 CNVSEEHEWNARLYAQDWIKESKEGYKQSDLASQC 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     454 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97000351; PubMed=8843436;
                                                                                           STRAIN-COLUMBIA;
MEDLINE-97471969; PubMed-9330910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PUTATIVE SECRETED PROTEIN.
                                                                                                                                                                                                                                                                                     34; Conservative
                                                                                                                                                                                          4:215-230(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces coelicolor.
                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=A3(2)
                                                                                                                                                                               clones.";
                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                             DNA Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O9KZR1
                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09KZR3
```

g

Д οχ

ŏ

ŏ

```
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 EA-MGDIFPDADADEDSLAGELD-----EAMGSSEWLALIKSPQAFYRGRPSWQGTPGV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169 DAEAGDIEDGI----RDLLAAEADWRASDAYAQDRAHWLATPRHIPVILAGITA-PGAPGA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110 ARPLDV-TCGRPLFTQALFTLGPGRHRWFQHVHHLLLDGYGFRLVAERVAAAYRAGAEAG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----RSDILAH 60
                                                                                                                                               210 VTAVAYTTPTPYWRYLTALDVLSHEADGTVVAFGDSITDGARSQSDANHRWTDVLAARLH 269
                                                                                               40 IRAVIFTCGGSRWR---RSDILAHE-----AMGDTFPD-----ADADE---DSLAGELD 82
                                                       37; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces pristinaespiralis.
Bacteria; Firmioutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-97158664; PubMed-9006024; MEDLINE-97158664; PubMed-9006024; De Crecy-Lagard V., Blanc V., Gil P., Naudin L., Lorenzon S., Pamechon A., Bamas-Jacques N., Crouzet J., Thibaut D.; Pamechon A., Bamas-Jacques N., Crouzet J., Thibaut D.; Pameshinamycin I biosynthesis in Streptomyces pristinaespiralis: "Pristinamycin I biosynthesis in Streptomyces pristinaespiralis: molecular characterization of the first two structural peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    de Crecy-Lagard V.A., Saurin W., Thibaut D., Gil P., Naudin L., Crouzet J., Blanc V.; Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                83 EAMGS-----SEWLA----LTKSPQAFYRGRPSWQGTPGVLRGSRDVL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 78; DB 2; Length 2591;
Pred. No. 75;
10.3%; Score 78.5; DB 2; Length 454; 31.0%; Pred. No. 8.5; tive 12; Mismatches 29; Indels 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79477DDA3715D6A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                             PRT; 2591 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001242; DUF4.
InterPro; IPR003880; Phosphopant_attach.
Pfam; PF00501; AMP-binding; 2.
Pfam; PF00668; Condensation; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 AAPYGVRLCGREFIRAVIFTCGGSRWR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50075; ACP_DOMAIN; 2.
PROSITE; PS00455; AMP_BINDING; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2591 AA; 276024 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacterioí. 179:705-713(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, X98690; CAA67248.1; --
EMBL, Y11548; CAA72311.1; --
HSSP, P14687; 1AMU.
InterPro; IPR000873; AMP-bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF00550; pp-binding; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00154; AMPBINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 LR----GSRDVLAGLSS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRISTINAMYCIN I SYNTHASE I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phosphopantetheine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity
Matches 38; Conserv
                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                synthetase genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=38300;
                                                                                                                                                                                                                                                                                                                                                                                                              054959; 005632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-SP92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
```

Search completed: June 27, 2002, 16:16:28 Job time: 497 sec

.

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on:

June 27, 2002, 16:08:46 ; Search time 18.68 Seconds (without alignments) 294.335 Million cell updates/sec

US-09-781-077-2 760 Title: Perfect score: Sequence:

1 MARYMLLLLLAVWVLTGELW......GLSSSCCKWGCSKSEISSLC 142

Scoring table:

105224 seqs, 38719550 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

S
闰
H
24
Æ
Σ
Σ
₽
S

		Description		Opril 2 Squalus aca				Q9trm8 canis famil	P22969 equus cabal	P04090 homo sapien	pan t	P01348 sus scrofa	pos		097937 callithrix	4	P11952 raja erinac	O9wuk0 rattus norv		P51460 homo sapien			_			Q9wv41 rattus norv		_	064171 mesocricetu		σ,	o pan			PSIUZS Oreochromis O9V581 homo sanien	
SUMMARIES		ID	1	INL5 MOUSE	INLS HIMAN	RELX ODOTA	BELY CAMEA	PELY HOPER	DEL 2 HINGS	NELZ_HUMAN	DELY DIC	TMI 2 DOUTES			DELY MACMI	DET V DA TER	TNI 2 DAM	INI.3 MOTOR	TNI 3 HIMAN	PELY MOHER	REL HIMAN	RELY DAY	PET.1 DANTE	TNL1 PROME	TNI G PAT	LIRP LOCKT	INTE MOUSE	RELX MEGALI	RELH RABIT	TNC HIMAN	TNS DANIED	INS PIG	TNS MACES	INS ORENI	INL6_HUMAN	
		BB																													ı ,				1	
		Length	54	135	135	44	177	182	185	166	182	132	131	131	185	64	105	122	131	185	185	186	166	134	188	145	191	177	178	110	110	108	110	113	213	
dР	Query	Match	20.1	m	16.6	10	-	-	_			13.6	13.4	13.4	13.4	13.2	13.2	13.2	13.0	13.0	13.0			11.6	11.6	11.6	11.6	11.4				0	٥.	10.6	Ö	
	i	Score	153	148	126.5	117	112.5	110	109.5	108.5	106.5	103.5	102	101.5	101.5	100.5	100.5	100	66	66	98.5	86	95.5	88.5	88.5	88	88	86.5	86.5	84.5	83.5	81.5	80.5	80.5	80	
	Result	NO.	н (

opter ithec is pis trivi glut ichia acter opter omyce omyce omyce																
balaenopter cercoptithec lophius pis actus trivi myxine glut escherichia rhodobacter palaenopter gallus gall streptomyce octodon deg			thyes;	Б Б.,	> I	IS NOT							Gaps	1	29	
P11184 P30407 P01341 P01341 P10604 P07604 P37743 P11185 P011332 P011332 P011312			Chondrichthyes lus.	O'Byrne	from spiny	SPECIES INKED BY	, ,						;	EAMGSS	143	54
	TS	4 AA. ate)	or annocation update) dogfish). lata; Craniata; Vertebrata; Choi Squaloidei; Squalidae; Squalus	Steinetz B.G.,	ce of relaxin	AN A CHAIN L	rted. INSULIN/IGF/RELAXIN FAMILY			CHAIN.	RELAXIN A CHAIN. PYRROLIDONE CARBOXYLIC ACID INTERCHAIN. INTERCHAIN.	2A5B CRC64;	DB 1; Length 54 .3e-08; es 4; Indels	ā	CCKWGCSKSET	
X_BALAC CERAE LIOPPI AOTTR MYXGL RECOLI A_RHCA CHICK CHICK CICK CICK COTDE	ALIGNMENTS	Ω,	on un ata; ; squ	, C	sequence	IN AND	I/NI	axin		m	A CEDONE AIN.	73AD3	53; 5. 1. atche	AMGDT	CLSS	: GMSSI
RELX_BALAC INS_CERAE INS_LOPPI INS_ACTTR INS_AVXGL TYRR_ECOLI CATA_RHOCA RELX_BALED INS_CHICK INS_CHICK INS_CHICK INS_CTDE INS_CTDE	ALIC	PRT; ed) sequence	dogfish). ata; Craniata Squaloidei;	ed=3780747; L.K., Schwabe	the ; 1986) RELA		o o	_IGF_relaxin		RELAXIN	RELAXIN A OPYRROLIDON) INTERCHAIN INTERCHAIN	1B7206773AD32A5B	Score 153; DB Pred. No. 1.3e 0; Mismatches	SDILAHE	KGSRDVL#	
ппппппппппппппппппппппппппппппппппппппп		ш	dog dog Jata Squ	.378 K.,	and (3) 1, 3, 1, 1) N OF	OF A	0		. 1.				→	WRRS	GVLF	
54 110 110 1108 1115 513 576 576 107 1109		æ,	Spi (Spi ; Ch ale	5; PubMed=	cation, canthia 51:335- FUNCTIC	DDIMER		; ; Insulin llin; 1.	GF; 1. INSULIN;	30	54 1 1 4 1 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	5910 MW	20.1%; 28.6%; ative	TCGGSR	SWQGTP	: : -WEGSP
10.3 100.3 100.1 100.1 10.0 9.7 9.7		(Re	acanthias a; Metazoa anchii; Squ	(4035; E., G	, purificalus achem. 16	N. HETERCE RONDS	LAR LOC TY: BEI A26463 B26463	, 6RLX. R000739	M00078; IlGF; 1. PS00262; INSULI family; Hormone	30	31 13 255	AA;	Similarity 28. 2; Conservative	FIRAVIE 	AFYRGRE	
78.5 78.5 76.5 76.5 76.5 73.5 73.5 73.5		LT 1 SQUAC RELX_SQUAC P11953; 01-0CT-1989 01-PE-1989 16-0CT-2094	Relaxin. Squalus acanthia Eukaryota; Metaz Elasmobranchii;	[1] SEQUENCE. TISSUE=OVARY; MEDLINE=87054035; Bullesbach E.E., (Callard I.P.	"Isolation, purification, and doglish (Squalus acanthias)." Eur J. Blochem. 161:335-341(? 	YET KNOWN. SUBUNIT: HETERODIMER DISULFIDE RONDS	-!- SUBCELLULAR LOCATION -!- SIMILARIY: BELONGS : PIR; A26463; A26463. PIR; B26463: R26463.	P04090 Pro; IP	SMART; SM00078; PROSITE; PS0026 Insulin family;	CONS	IN RES ILFID ILFID	NCE 54	h Simi 32;	GVRLCGREFIRAVIFTCGGSR ::	ALTKSPQ	
44444444444444444444444444444444444444		RESULT 1 RELX_SQUAC ID RELX_ AC P1195 OT 01-F91	Relaxin. Squalus Eukaryot Elasmobr	(1) SEQU TISSI MEDL Bull Call	"Iso dogf Eur.		-!- -!- PIR; PIR;	HSSP; Inter Pfam;	SMART PROSI Insul	CHAIN NON_C	CHAIN MOD_RES DISULFID DISULFID	SEQUENCE	Query Match Best Local Matches	31 0	91 1	30 -
		RES REI ID AC DT DT	OS OC OS	RN RZ RX RA	RT RE CC					FT	FT FT FT	So	Qu Bee	Qy Dp	Qy	Ωp

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its modified non-priofit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lok S., Jaspers S.; "Identification of INSL5, a new member of the insulin superfamily.";
                                                                                                                                                                                                                                                        Conklin D., Lofton-Day C.E., Haldeman B.A., Ching A., Whitmore T.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MAY HAVE A ROLE IN GUT CONTRACTILITY OR IN THYMIC DEVELOPMENT AND REGULATION.
-!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                          "Cloning of two novel mammalian paralogs of relaxin/insulin family proteins and their expression in testis and kidney."; Mol. Endocrinol. 13:2163-2174(1999).
                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INSULIN-LIKE PROTEIN INSL5 B CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INSULIN-LIKE PEPTIDĖ INSL5 A CHAIN
                                                230-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
1nsulin-like peptide INSL5 precursor (Insulin-like peptide 5):
(Relaxin/insulin-like protein) (Relaxin/insulin-like factor 2).
INSLS OR ZINS3 OR RIF2 OR RIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
CONNECTING PEPTIDE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05FF9A0F613DBF92 CRC64;
                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR000739; Insulin_IGF_relaxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; APO54842; AAF09093.1; ALT_INIT.
EMBL; AF054843; AAF09094.1; --
EMBL; BC010968; AAH10968.1; --
                      PRT;
                                                                                                                                                                                                                                                                                                                                                          STRAIN=FVB; TISSUE=Ovary;
MEDLINE=20065648; PubMed=10598589;
                                                                                                                                                                                                                                                  MEDLINE=99389725; PubMed=10458910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insulin family; Hormone; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF133817; AAD29687.1; -. EMBL; AF076971; AAD48089.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 B
15524 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00078; IIGF; 1.
PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGI:1346085; Insl5.
                                                                                                                                                                                                                                                                                                             Genomics 60:50-56(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22
135
                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
135 AA;
                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N. A.
                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49
115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rissue=Colon
                           INL5 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROPEP
RESULT 2
INL5_MOUSE
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way undified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEVELOPMENT AND REGULATION.

-1- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO DISULEIDE BONDS (BY SIMILARITY).

-1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN RECTUM WITH LOWER LEVELS IN UPERUS AND ASCENDING AND DESCENDING COLON.

-1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                   50 --LEGHFHSQOAETRNYLOLLDRHEPSKKTLEHSLPKTDLSGOELVRDPQAPKEG--LWE 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lok S., Jaspers S.;
"Identification of INSL5, a new member of the insulin superfamily.";
Genemics 60:50-56(1999).
-i- FUNCTION: MAY HAVE A ROLE IN GUT CONTRACTILITY OR IN THYMIC
                                                                                                                                    61 EAMGDIFPDADADEDSLAGELDEAMGSSEWL------ALIKSPQAFYRGRPSWQ 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUB-Colon;
BEDLINE-99389725; PubMed=10458910;
Conklin D., Lofton-Day C.E., Haldeman B.A., Ching A., Whitmore T.E.,
                                                                 1 MARYMLLLLLAVWVLTGELWPGAEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAH 60
                                                                                     51; Indels 36; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONNECTING PEPTIDE (POTENTIAL).
INSULIN-LIKE PEPTIDE INSLS A CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INSULIN-LIKE PEPTIDE INSL5 B CHAIN
                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Insulin-like peptide INSL5 precursor (Insulin-like peptide 5).
19.5%; Score 148; DB 1; Length 135; 29.9%; Pred. No. 1.1e-07; tive 21; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERCHAIN (BY SIMILARITY). INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98FFCB20E9C4BC1F CRC64;
                                                                                                                                                                                                           109 GTPGVLRGSRDVLAGLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                               106 LKKHSVVSRRD----LQALCCREGCSMKELSTLC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000739; Insulin_IGF_relaxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00262; INSULIN; 1.
Insulin family; Hormone; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF133816; AAD29686.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 126 E
135 AA; 15318 MW;
                                           46; Conservative
                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00078; ILGF; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
            Query Match
Best Local Similarity
Matches 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49
115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                       INL5_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                     INL5_HUMAN
                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                      δλ
                                                                                                                                                     Óλ
```

----- 23

93 LTKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCCKWGCSKSEISSLC 142

1 QLCGRGFIRALIFACGGSRWATS-----

δý

g

Canis familiaris (Dog). Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Carnivora, Fissipedia, Canidae, Canis.

16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)

Prorelaxin precursor.

STANDARD;

Q9TRM8; Q9TRM9; Q9N0Z7;

RELX_CANFA

RELX_CANFA

```
5,
                                                                                                       71 DAD-EDSLAGELDEAMGSSEWLALTKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCC 129
                                                                                                                                86 DASGEDRLWG------GOMPTEELWKSKKHSVMSRQD------LOTLCC 122
                                     45; Gaps
                                                  32 VRLCGREFIRAVIFTCGGSRWRR-----SDILAH-----EAMGDTFPDA 70
                                                                            26 VRLCGLEYIRTVIYICASSRWRRHLEGIPQAQQAETGNSFQLPHKREFSEENPAQNLPKV 85
                                                                                                                                                                                                                                                                                                                                     Odontaspis taurus (Sand tiger shark) (Eugomphodus taurus).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Galeomorphii; Galeoidea; Lamniformes; Odontaspididae;
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-82004703; PubMed=7274472; Gowan L.K., Reinig J.W., Schwabe C., Bedarkar S., Blundell T.L.; on the primary and tertiary structure of relaxin from the sand tiger shark (Odontaspis taurus)."; FEBS Lett. 129:80-82(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bullesbach E.E., Gowan L.K., Schwabe C., Steinetz B.G., O'Byrne E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Isolation, purification, and the sequence of relaxin from spiny dogfish (Squalus acanthias).";
Eur. J. Blochem. 161:335-341(1986).
-1- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
          DB 1; Length 135;
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
6122F6604C660607 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PYRROLIDONE CARBOXYLIC ACID.
 16.6%; Score 126.5; DB 1; 30.8%; Pred. No. 1.3e-05; tive 8; Mismatches 39;
                                                                                                                                                                                                                                                                              1-JUL-1986 (Rel. 01, Created)
01-CCT-1989 (Rel. 12, Last Sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RELAXIN B CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RELAXIN A CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPRO00739; Insulin_IGF_relaxin.
Pfam; PF00049; Insulin; 1.
SMART; SM00078; IIGF; 1.
PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=87054035; PubMed=3780747;
                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4730 MW;
                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                            123 TDGCSMTDLSALC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insulin family; Hormone.
                                                                                                                                                            130 KWGCSKSEISSLC 142
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                           Relaxin (Fragments).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A01616; RXRKOT.
                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=30501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 AA;
                         41;
                                                                                                                                                                                                                                                       RELX_ODOTA
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_CONS
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_CONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOD_RES
                                                                                                                                                                                                                                          RELX_ODOTA
                                                   ò
                                                                            qq
                                                                                                                                g
                                                                                                       δ
                                                                                                                                                                                   qq
                                                                                                                                                           ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way entities and this statement is not removed. Usage by and for commercial or send an email to license@isb-sib.ch).
                                                                                                                                                                                         Klonisch T., Hombach-Klonisch S., Froehlich C., Kauffold J.,
Steger K., Steinetz B.G., Fischer B.,
"Canine preprorelaxin: nucleic acid sequence and localization within
                                                                                                                                                                                                                                                                                                                        Stewart D.R., Henzel W.J., Vandlen R.;
"Purification and sequence determination of canine relaxin.";
"I Frotein Chem. 11:247-253(1992).
"I FOWGTION: Relaxin is an ovarian hormone that acts with estrogen to produce dilatation of the birth canal in many mammals.
"SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONNECTING PEPTIDE (BY SIMILARITY). RELAXIN A CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 177;
                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Placenta; syncytiotrophoblast.
-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   I -> S (IN REF. 2).
220BB0EC99DD302A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.8%; Score 112.5; DB 1
21.5%; Pred. No. 0.00041;
tive 16; Mismatches 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RELAXIN B CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000739; Insulin_IGF_relaxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERCHAIN
                                                                                                                                                             TISSUR=Placenta;
MEDLINE=99150177; PubMed=10026098;
                                                                                                                                                                                                                                                                                            TISSUE=Placenta;
MEDLINE=93000391; PubMed=1388669;
                                                                                                                                                                                                                                                    Biol. Reprod. 60:551-557(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SMU0078; ILGF; 1.
PROSITE; PS00262; INSULIN; 1.
Insulin family; Hormone; Signal.
                                                                                                                                                                                                                                                                                SEQUENCE OF 26-60 AND 154-177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF233687; AAF60302.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20563 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00049; Insulin; 1.
SMART; SM00078; ILGF; 1.
                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                      the canine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
```

```
33 RLCGREFIRAVIFTCGGSRWRRSDILAHEAMGDTFPDADADEDSLAGELDEAMGSSEWLA 92
                            ..... .....
```

81; Gaps

e0; Indels

43; Conservative

Matches

1;

:99

Score 117; DB 1; Length 44; Pred. No. 3.3e-05; 6; Mismatches 11; Indels

15.4%; 24.5%;

Similarity

Query ... Best Local Simi

Conservative

õ

```
g
                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                δ
DR
DR
DR
DR
DR
ET
FT
FT
FT
FT
SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              this SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Klonisch T., Ryan P.L., Yamashiro S., Porter D.G., Partial complementary deoxyribonucleic acid cloning of equine relaxin messenger ribonucleic acid, and its localization within the equine placenta!
                                                                                                                      98 RIATRSGKEKLLRELHFVLEDSNLNLEEMKKTFLNTQFEAEDKSLSKLDKHPRKKRDNYI 157
                                                                                                  ....-RGSRDVLA 122
                                                      61 EAMGDTFPDADADEDSLAGELDEAMGSSEWLA-----LIKSPQAFYRGRPSWQGTPGVL 114
                                                                           55 ------AGQLRERRQISEPLAEVVPSSIINDPEILSLMLQSIPGMPQEL 97
          1 MARYMLLLLLAVWVLTGELWPGAEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSD1LAH 60
                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                 1 MLRWFLSHLIGVWLLLSQL-PREIPATDDKKLKACGRDYVRLQIEVCGSIWWGRK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                  STRAIN-HOKKAIDO; TISSUB-Placenta;
Min K., Shiota K., Ogawa T.;
"Molecular cloning of equine preprorelaxin cDNA.";
J. Reprod. Dev. 42:171-178(1996).
                                                                                                                                                                                                                                      782269; Q28907;
01-ANG-1991 (Rel. 19, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                          PRT; 182 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Placenta;
MEDLINE=91275796; PubMed=2055195;
                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Placenta;
MEDLINE=95359320; PubMed=7543295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol. Reprod. 52:1307-1315(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB000201; BAA19069.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 26-53 AND 163-182.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; S78800; AAB35036.1; -. PIR; A49739; A49739. PIR; B49739; B49739.
                                                                                                                                                 123 GLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                              SEQUENCE OF 32-174 FROM N.A.
                                                                                                                                                                                                                                                                                  Prorelaxin precursor (RXN).
                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                        Equus caballus (Horse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P01348; 4RLX.
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9796;
                                                                                                                                                                                                                              RELX_HORSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               placenta.
                                                                                                                                                                                                                       RELX_HORSE
                                                                                                                                                                                                                                 a
                                                                                      g
                                                                                                                               g
                                                                                                                                                      ŏ
```

```
Hudson P., John M., Crawford R., Haralambidis J., Scanlon D., Gorman J., Tregear G., Shine J., Niall H.; "Relaxin gene expression in human ovaries and the predicted structure of a human preprorelaxin by analysis of cDNA clones."; EMBO J. 3:2332-2339(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 EAMGDTFPDADADE-----DSLAGELDEAMGSSEWL--ALTKSPQAFYRGR-PSW----- 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 E-----PGLEAGQPVEIVSSSISKDAEALNTKLGLNSNLPKEQKATLSERQPSWRELLQ 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 QPALKDSNLNLEEFEFTILKTQSEVEDDSLSELKNLGLDKHSRKKRMIQLSHKCCYWGCT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MARYMLILLLAVWVLTGELWPGAEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MRRIFLSHVLGAWLILSQLPRELSGQKPDDVIKACGRELARLRIEICGSLSWKKTVLRLE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gunnersen J.M., Fu P., Roche P.J., Tregear G.W.;
"Expression of human relaxin genes: characterization of a novel
alternatively-spliced human relaxin mRNA species.";
Mol. Cell. Endocrinol. 118:85-94(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PARTIAL SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE
                                                                                                                                                                                                                                                                                                                                                               14.5%; Score 110; DB 1; Length 182; 21.8%; Pred. No. 0.00074; tive 25; Mismatches 70; Indels :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY. MEDLINE-85051298; PubMed-6548702;
                                                                                                                                                                                          INTERCHAIN (BY SIMILARITY). INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                           BY SIMILARITY.
A -> V (IN REF. 2).
L -> Q (IN REF. 2).
; E5C9414303A838B8 CRC64;
                                                                                                                                                     CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT, 185 AA. STANDARD, PRT; 185 AA. P04090; Q9UCX3; Q99936; 01-NOV-1986 (Rel. 03, Last sequence update) 01-NOY-1986 (Rel. 03, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                              RELAXIN A CHAIN.
                                                                                                                             RELAXIN B CHAIN
InterPro; IPR000739; Insulin_IGF_relaxin. Pfam; PF00049; Insulin; 1. SWART; SM00078; IIGF; 1. SPS027E; PS00262; INSULIN; 1. Insulin.family; Hormone; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96328899; PubMed=8735594;
                                                                                                                                                                                                                                                                                         133 L
20721 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                       41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prorelaxin H2 precursor.
                                                                                                                                                            156
182
169
182
173
66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                         54
161
35
17
47
168
168
133
182 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135 KSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Prostate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175 RKELAROC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sehra H.;
                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                      SIGNAL
                                                                                                                                                                   PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REL2_HUMAN
                                                                                                                                              CHAIN
                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is along as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                           -1- SUBCELLULAR LOCATION: Secreted.
-1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are produced by alternative splicing.
-1- TISSUE SPECIFICITY: Expressed in the ovary during pregnancy. Also expressed in placenta, decidua and prostate.
-1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                 MEDLINE-92241162; PubMed=1572287;
Winslow J.W., Shih A., Bourell J.H., Weiss G., Reed B., Stults J.T.,
Goldsmith L.T.;
                                                                                                                                                       Human seminal relaxin is a product of the same gene as human luteal
                        Buellesbach E.E., Schwabe C., "Total synthesis of human relaxin and human relaxin derivatives by solid-phase peptide synthesis and site-directed chain combination." J. Biol. Chem. 266:10754-10761(1991).
                                                                                                                                                                                                                     MEDLINE=91167739, PubMed-2076464; Winslow J.W., Griffin P.R., Rinderknecht E., Vandlen R.L.; "Structural characterization by mass spectrometry of native and recombinant human relaxin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00262; INSULN; 1.
Insulin family; Hormone; Multigene family; Signal; 3D-structure;
Alternative splicing.
SIGNAL
SIGNAL
25 53 RELAXIN B CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biomed. Environ. Mass Spectrom. 19:655-664(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RELAXIN B CHAIN.
CONNECTING PEPTIDE.
RELAXIN A CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000739; Insulin_IGF_relaxin.
                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERCHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERCHAIN
            MEDLINE=91250367; PubMed=2040595;
                                                                                                                                                                                Endocrinology 130:2660-2668(1992).
                                                                                                                                                                                                         SEQUENCE OF 25-53 AND 162-185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X00948; CAA25460.1; --
EMBL; AL135786; CAC04177.1; --
EMBL; AL135786; CAC04176.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; 583200; AAD14429;;;
EMBL; A17315; CAA01334;;
EMBL; A06925; CAA00602.1;;
PIR; A60982; A60982.
                                                                                        PARTIAL SEQUENCE OF 25-51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00049; Insulin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00078; IIGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179740; -
                                                                                                                                                                       relaxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOD_RES
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
```

```
EIVPSFINKDTETINMMSEEVANLPQELKLTLSEMQPALPQ
LQQHVP -> GDFIQTVSLGISPDGGKALRTGSCFTREFLG
ALSKLCHPSSTKIQKP (IN ISOFORM 2).
MISSING (IN ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DAPQTPRPVAEIVPSFINKDTETINMMSEFVANLPQELKITLSEWQPALPQLQQHVPVLK 120
                                                                                                                                                                                                                                                                                                                                                   121 DSSLLFEEFKKLIRNRQSEAADSSPSELKYLGLDTHSRKRRQLYSALANKCCHVGCTKRS 180
                                                                                                                                                                                                                                                                                                                                ------AFYRGRPS-------WQGTPGVLRGSRDVLAGLSSSCCKWGCSKSE 137
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                   1 MARYMLLLILLAVWVLTGELWPGAEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAH 60
                                                                                                                                                                                                                                                         1 MPRLFFFHLLGVCLLLNQFSRAVADSWMEEVIKLCGRELVRAQIAICGMSTWSKRSLSQE 60
                                                                                                                                                                                                                                                                                  61 EAMGDIFPDADADEDSLAGELDEAMGSSEWLA------LTKS-----PQ----- 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                        43;
                                                                                                                                                                                        14.4%; Score 109.5; DB 1; Length 185; 22.7%; Pred. No. 0.00084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- SUBCELLULAR LOCATION: Secreted.
-!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PARTIAL SEQUENCE FROM N.A. (ISOFORM 2), AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                    78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Evans B.A., Fu P., Tregear G.W.; "Characterization of two relaxin genes in the chimpanzee."; J. Endocrinol. 140:385-392(1994).
                                                                                                                                                    21042 MW; AC73DBDE2090091B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FELL PANTR STANDARD; PRT; 166 AA. P51455; P79267; 01-0CT-1996 (Rel. 34, Created) 01-0CT-1996 (Rel. 34, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                 22.7%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prorelaxin H2 precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Placenta;
MEDLINE=94238260; PubMed=8182365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pan troglodytes (Chimpanzee).
                                                                                                                                                                                                                  Conservative
                                                                                                                                                    185 AA;
                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9598;
                                                                                                                                                                                                                                                                                                                                                                              138 ISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                    181 LARFC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNL2 OR RLX2
                                                                                                                                                                                                               42;
  DISULFID
            VARSPLIC
                                             VARSPLIC
                                                                                                                                                    SEQUENCE
                                                                                                                                                                                       Query Match
                                                        HELIX
STRAND
                                                                                                                  STRAND
                                                                                                                             HELIX
                                                                                          HELIX
                                                                                HELIX
                                                                                                        TURN
                                                                                                                                          IURN
                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                REL2_PANTR
FT
FT
FT
FT
FT
FT
SQ
                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                     Db
                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dp
```

```
PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PDB;
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                           EIVPSFINKDTETINMMSEFVANLPQELKLTLS -> DFIQ
                                                                                                                                                                                                                                                                                                                                                                                                                        TVSLGISPDGGKALRTGSCFTREFLGALS (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92 A-----LTKS-----PQ-----WQ 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 ANLPQELKLILSEMQPALPQLQQYVPVLKDSSLLFEEFKKLIRNRQSEAADSSPSELKYL 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55; Indels 43; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 VRLCGREFIRAVIFTCGGSRWRRSDILAHEAMGDTFPDADADEDSLAGELDEAMGSSEWL 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 IKLCGRELVRAQIAICGKSTWSKRSLSQEDAPQTPRPVAEIVPSFINKDTETINMMSEFV 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-87308187; PubMed-2442155;
Haley J., Crawford R., Hudson P., Scanlon D., Tregear G., Shine J.,
produced by alternative splicing.
TISSUE SPECIFICITY: EXPRESSED IN THE CORPUS LUTEUM OF PREGNANCY
AND IN THE PLACENTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                      SMART; SM00078; IlGF; 1.
PROSITE; PS00262; INSULIN: 1.
Insulin family; Hormone; Multigene family; Signal; Polymorphism;
Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.3%; Score 108.5; DB 1; Length 166; 23.4%; Pred. No. 0.00094; tive 20; Mismatches 55; Indels 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              KSTWS -> MSTLG (IN SOME ALLELES).
220851E3134CEBDB CRC64;
                                                                                                                                                                                                                                                                                                                    POTENTIAL.

RELAXIN B CHAIN (PROBABLE).

CONNECTING PEPTIDE (PROBABLE).

RELAXIN A CHAIN (PROBABLE).

INTERCHAIN (BY SIMILARITY).

INTERCHAIN (BY SIMILARITY).
                                           -! - SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISSING (IN ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1989 (Rel. 11, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 GTPGVLRGSRDVLAGLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY
                                                                                                                                                                                                                      InterPro; IPR000739; Insulin_IGF_relaxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166 AA; 18760 MW;
                                                                                                                                                                                  EMBL; Z27245; CAA81758.1; -.
                                                                                                                                                                                                 AAD14430.1; -.
                                                                                                                                                                                                                                         Pfam; PF00049; Insulin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                  34
138
166
153
166
157
157
                                                                                                                                                                                                                                                                                                                                                                                                                                                          166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-1989 (Rel. 11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prorelaxin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  scrofa (Pig).
                                                                                                                                                                                                                  6RLX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            85
30
                                                                                                                                                                                                                  HSSP; P04090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RELX_PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                      VARSPLIC
                                                                                                                                                                                                                                                                                                              NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Niall
                                                                                                                                                                                                                                                                                                                                                  PROPEP
                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
```

ŏ 임 ð

ò

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i-FUNCTION: RELAXIN IS AN OVARIAN HORMONE THAT ACTS WITH ESTROGEN TO PRODUCE DILATATION OF THE BIRTH CANAL IN MANY MAMMALS.
-i-SUBDNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schwabe C., McDonald J.K.; "Demonstration of a pyroglutamyl residue at the N terminus of the B-chain of porcine relaxin."; Biochem. Biophys. Res. Commun. 74:1501-1504(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isaacs N.W., James R., Niall H., Bryant-Greenwood G., Dodson G.G., Evans A., North A.C.T.; "Relaxin and its structural relationship to insulin."; Nature 271:278-281(1978).
                                                                                                                                                                                                                                                                                                                                                                    James R., Niall H., Kwok S., Bryant-Greenwood G.; "Primary structure of porcine relaxin: homology with insulin and
                                                                                          SEQUENCE FROM N.A.
MEDLINE=83157118; PubMed=6897721;
Haley J., Hudson P., Scanlon D., John M., Cronk M., Shine J.,
Tregear G., Niall H.;
Tregear G., Niall H.;
Porcine relaxin: molecular cloning and cDNA structure.";
DNA 1:155-162(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- SUBGELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-76231539; PubMed-938497; Schwabe C., McDonald J.K., Steinetz B.G.; Primary structure of the A chain of porcine relaxin."; "Primary structure of the A chain of porcine relaxin."; Plochem. Blophys. Res. Commun. 70:397-405(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schwabe C., McDonald J.K., Steinetz B.G.; "Primary structure of the B-chain of porcine relaxin."; Biochem. Biophys. Res. Commun. 75:503-510(1977).
"Porcine relaxin. Gene structure and expression.";
J. Biol. Chem. 262:11940-11946(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-77236040; PubMed=887933;
Schwabe C., McDonald J.K.;
"Relaxin: a disulfide homolog of insulin.";
Science 197:914-915(1977).
                                                                                                                                                                                                                                                                                                            PRELIMINARY SEQUENCE OF 25-54 AND 161-182.
MEDLINE-77213067; Pubmed-876374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=78092399; PubMed=622170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=77157271; PubMed=851452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=77134136; PubMed=843375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; K01088; AAA31114.1; --
EMBL; J02792; AAA31115.1; --
EMBL; A16593; CAA01295.1; --
EMBL; A06652; CAA00600.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                 related growth factors.";
Nature 267:544-546(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8]
3D-STRUCTURE MODELING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2RLX; 15-OCT-94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1RLX; 15-OCT-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A29796; A29796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 161-182.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A01615; RXPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 25-51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 25
```

```
.;
m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Leydig insulin-like peptide precursor (Ley-I-L) (Relaxin-like factor).
                                                                                                                                                                                                                                                                                                                                                                                                                                  69 DADA------DEDSLAGELDEAMGSSEWLALTKSPQAFYRGRPSWQ------- 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----GTPGVLRGSRDVLAGLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                              14.0%; Score 106.5; DB 1; Length 182;
21.7%; Pred. No. 0.0016;
tive 22; Mismatches 68; Indels 51; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 FEEFKKIILNRQNBABDKSLLELKNLGLDKHSRKKRLFRMTLSEKCQVGCIRKDIARLC 182
                                                                                                                                                                                                                                                                                                                                                                     9 LLAVWVLTGELWPGAEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAHEAMGDTFP 68
                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Testis;
MEDLINE-97107158; PubMed-8949906;
Bathgate R.A.D., Balvers M., Hunt N., Ivell R.;
"Relaxin-like factor gene is highly expressed in the bovine ovary of the cycle and pregnancy: sequence and messenger ribonucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBUNT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO DISULFIDE BONDS (BY SIMILARITY).
-!- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN LEYDIG CELLS.
-!- SIMILARITY: BELONGS TO THE INSULIN/TGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol. Reprod. 55:1452-1457(1996).
-1- FUNCTION: COULD PLAY A ROLE IN TESTICULAR FUNCTION AND
                                                                                                               CONNECTING PEPTIDE.
RELAXIN A CHAIN.
PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                   WGRT -> TWGR (IN REF. 3).
S -> L (IN REF. 1).
Q -> E (IN REF. 6).
20736BB089F13AB4 CRC64;
                                                                                                                                                                                                        G -> GVWS (IN REF. 4).
                                                              Insulin family; Hormone; Signal; 3D-structure.
                                                                                                  RELAXIN B CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 AA
InterPro; IPR000739; Insulin_IGF_relaxin.
Pfam; PF00049; Insulin; 1.
SMART; SM00078; IIGF; 1.
PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                             INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                    20818 MW;
                                                                                                                                                                                                                                                                                                                                           39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                            154
182
25
169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INL3_BOVIN
                                                                                                                                        MOD_RES
DISULFID
                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                   CONFLICT
                                                                                                            PROPEP
                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
INL3_BOVIN
                                                                                                                                                                                                                                                                                                                                         Matches
 DR
DR
DR
ET
FT
FT
FT
FT
FT
FT
FT
FT
SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ολ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
```

```
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Leydig insulin-like peptide precursor (Ley-I-L) (Relaxin-like factor).
                                                                                                                                                                                                                                                                                                                                                                                              80 E--LDEAMGSSE---WLALTKSPQA--FYRGRPSWQGTPGVLRGSRDVLAGLSSSCCKWG 132
                                                                                                                                                                                                                                                                                                                                                                                                                           74 QHLLHGLWASGDPVLVLAPQPLPQASRHHHHRRATAINP-----ARHCCLSG 120
                                                                                                                                                                                                                                                                                                               33; Gaps
                                                                                                                                                                                                                                                                                                                                   23 AEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAHEAMGDTFPDADADEDS---LAG 79
                                                                                                                                                                                                                                                                                                                                                     Adham I.M., Burkhardt E., Benahmed M., Engel W.;
"Cloning of a cDNA for a novel insulin-like peptide of the testicular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Structural organization of the porcine and human genes coding for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leydig cell-specific insulin-like peptide (LEY I-L) and chromosomal localization of the human gene (INSL3)."; (Genomics 20:13-19(1994).
                                                                                                                                     LEYDIG INSULIN-LIKE PEPTIDE B CHAIN.
C PEPTIDE (POTEWRIAL).
LEYDIG INSULIN-LIKE PEPTIDE A CHAIN.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Manmalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Burkhardt E., Adham I.M., Brosig B., Gastmann A., Mattei M.-G.,
                                                                                                                                                                                                                                                                           13.6%; Score 103.5; DB 1; Length 132; 28.5%; Pred. No. 0.0023; Live 17; Mismatches 43; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN PRENATAL AND POSTNATAL LEYDIG CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: COULD PLAY A ROLE IN TESTICULAR FUNCTION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                               116 121 BY SIMILARITY.
132 AA; 14378 MW; A5585500C7F2241D CRC64;
                                        InterPro; IPR000739; Insulin_IGF_relaxin.
Pfam; PF00049; Insulin; 1.
SMART: SM00708; IIGF; 1.
PROSITE; PS00262; INSULIN; 1.
Insulin family; Hormone; Signal.
or send an email to license@isb-sib.ch).
                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol. Chem. 268:26668-26672(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFIDE BONDS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Testis;
MEDLINE=94075362; PubMed=8253799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE-94292172; Pubmed=8020942;
                           EMBL; AF094580; AAC63380.1;
                                                                                                                                                                                                                                                                   Query Match 13.6%
Best Local Similarity 28.5%
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                     57
104
132
117
130
                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 CSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 CTRODLLTLC 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPERMATOGENESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leydig cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INSL3 OR RLF
                                                                                                                                                                                  DISULFID
                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INL3_PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Engel W.;
                                                                                                                                                  PROPEP
                                                                                                                       SIGNAL
CC
CC
DR
DR
DR
DR
FT
FT
FT
FT
SO
                                                                                                                                                                                                                                                                                                                                                                                              Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΩD
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its work by non-profit institutions as long as its content is in no way undiffed and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zarreh-Hoshyari-Khah M., Einspanier A., Ivell R.;
Zarreh-Hoshyari-Khah M., Einspanier A., Ivell R.;
"Differential splicing and expression of the relaxin-like factor gene in reproductive tissues of the marmoset monkey (Callithrix jacchus).";
Biol. Reprod. 60:445-453(1999).
-:- FUNCTION: COULD PLAY A ROLE IN TESTICULAR FUNCTION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation update)
Leydig insulin-like peptide precursor (Ley-I-L) (Relaxin-like factor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --- SUBGNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO DISULETDE BONDS (BY SIMILARITY).
--- SUBCELLULAR LOCATION: Secreted.
--- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORY/TRUNCAFED FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
--- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN THE LEYDIG CELLS OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 ELL---QWLEGQHLFHGLMASGDPMLVLAPQPPPQAS-GHHHHRRAAATNPARHCCLSGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 EAMGSSEW-----LALIKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCCKWGC 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 AEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAHEAMGDTFPDADADEDSLAGELD 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 APAQEAP--EKLCGHHFVRALVRLCGGPRW-----SPEDGRAVAGGDR 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Callithrix jacchus (Common marmoset).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
                                                                                                                                                                                                                                                                                           LEYDIG INSULIN-LIKE PEPTIDE B CHAIN.
                                                                                                                                                                                                                                                                                                                C PEPTIDE (POTENTIAL).
LEYDIG INSULIN-LIKE PEPTIDE A CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; DB 1; Length 131; 0.0031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46; Indels
                                                                                                                                                                                                                                                                                                                                                  INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                     8AB718870859EF3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE-99115234; Pubmed=9916013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 131 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 0.00
19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY
                                                                                                                                                                                         IPR000739; Insulin_IGF_relaxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.4%; Score 102; 24.8%; Pred. No. 0
                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                               Insulin family; Hormone; Signal.
                                                                                                                                                                                                      Pfam; PF00049; Insulin; 1.
SMART; SM00078; IIGF; 1.
PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                           14134 MW;
                                                                                                                                                         EMBL; X73636; CAA52016.1; -. EMBL; X68369; CAA48449.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                 56
103
131
116
129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 SKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 TRODLLTLC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INSL3 OR RLF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INL3_CALJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Callithrix
                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                        PROPEP
                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
 δλ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE=90073957; PubMed=2590381;

MEDLINE=90073957; PubMed=2590381;

Crawford R.J., Hammond V.E., Roche P.J., Johnston P.D., Tregear G.W.;

Crawford R.J., Hammond V.E., Roche P.J., Johnston P.D., Tregear G.W.;

Crawford R.J., Hammond Y.E., Relaxin gene.";

J. Mol. Endocrinol. 3:169-174(1889).

- FRUNTION: RELAXIN IS AN OVARIAN HORMONE THAT ACTS WITH ESTROGEN TO

- FROUTION: RELAXIN IS AN OVARIAN HORMONE THAT ACTS WITH ESTROGEN TO

- FROUTION: THE BIRTH CANAL IN MANY MAMMALS. MAY BE

INVOLVED IN REMODELING OF CONNECTIVE TISSUES DURING PREGNANCY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 RRHLLYGLVANSEPA - PGGPGLQPMPQTSHHHRHRRAAASNPARYCCLSGCSQQDLLTL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92 -----ALTKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSS---CCKWGCSKSEISSL 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41; Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33 RLCGREFIRAVIFTCGGSRWRRSDILAHEAMGDTFPDADADEDSLAGELDEAMGSSEWL- 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32 KLCGHHFVRALVRVCGGPLW-STEARRPVAAGD------GEL-----LOWLE 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Graniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                       GELLOWLERRH -> ESHSAAQDGGQ (IN SHORT
                                                                                                                                                                                                                                                                                                                                     LEYDIG INSULIN-LIKE PEPTIDE B CHAIN.
C PEPTIDE (POTENTIAL).
LEYDIG INSULIN-LIKE PEPTIDE A CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 131;
-i- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                     INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISSING (IN SHORT ISOFORM).
685743CAEECF8731 CRC64;
                                                                                                                                                                                                                                                                                                         Hormone; Signal; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.4%; Score 101.5; DB 1
28.1%; Pred. No. 0.0035;
tive 13; Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 AA.
                                                                                                                                                                                                                                          Enterpro; IPR000739; Insulin_IGF_relaxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISOFORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MISSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                       EMBL; AJ011961; CAA09888.1; -.
EMBL; AJ011962; CAA09888.1; JOINED.
EMBL; AJ011961; CAA09889.1; -.
HSSP; P01315; 1ZEI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Macaca mulatta (Rhesus macaque).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1991 (Rel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14252 MW;
                                                                                                                                                                                                                                                                                          PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                              Pfam; PF00049; Insulin; 1.
SMART; SM00078; IIGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 28.18
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                              104
131
117
130
121
74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prorelaxin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                  25
58
107
34
46
116
64
                                                                                                                                                                                                                                                                                                                  Insulin family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RELX_MACMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 C 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 C 130
                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P19884;
                                                                                                                                                                                                                                                                                                                                                                     PROPEP
                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RELX_MACMU
                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pp
                g
```

```
4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----QAFYRGRPS--WQGTPGVLRG-----SRDVLAGLSSSCCKWGCSKSE 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MARYMLLLLLAVWVLTGELWPGAEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 EAMGDTFPDADADEDSLAGELDEAMGSSEWLA-----LTKSP-----97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Raja erinacea (Little skate).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
PROMOFING GROWTH OF PUBIC LICAMENTS AND RIPENING OF THE CERVIX SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bullesbach E.E., Schwage C., Callard I.P.;
Relaxin from an oviparous species, the skate (Raja erinacea).";
Biochem. Biophys. Res. Commun. 143:273-280(1987).
-!- SUBDMIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Elasmobranchii, Squalea, Hypnosqualea, Pristiorajea, Batoidea, Rajiformes, Rajidae, Raja.
NCBL_TaxID=7782;
                                                                                                                                                                                                                                                                                                                                POTENTIAL.

RELAXIN B CHAIN (PROBABLE).

CONNECTING PEPTIDE (PROBABLE).

RELAXIN A CHAIN (PROBABLE).

INTERCHAIN (BY SIMILARITY).

INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.4%; Score 101.5; DB 1; Length 185; larity 22.7%; Pred. No. 0.0051; Conservative 22; Mismatches 78; Indels 43
                                                                            I- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- SUBCELLULAR LOCATION: Secreted.
-i- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7E3C5D21B57E185C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY
                                                                                                                               PIR; A34936, A34936.
HSSP; P04090; GRLX.
HING-Pro; IPR000739; Insulin_IGF_relaxin.
Flam: PF00049; Insulin; 1.
SWART; SM00078; IIGF, 1.
PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR00739; Insulin_IGF_relaxin
Pfam: PF00049; Insulin; 1.
SMART; SM00078; ILGF; 1.
PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=87156758; PubMed=3827922;
                                                                                                                                                                                                                                                                                                         Hormone; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20895 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A29543; A29543.
HSSP; P04090; GRLX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                      23
56
161
151
35
171
171
185 AA;
                               SUBUNIT: HETEROL DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                      Insulin family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138 ISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 LAKFC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Ovary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RELX_RAJER
P11952:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S:
Matches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Relaxin.
                                                                                                                                                                                                                                                                                                                                                                                      PROPEP
                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
RELX_RAJER
ROLY_RAJER
AC PI1952
DT 01-0CT
DT 01-0CT
DT 01-0CT
DE Relaxi
OC Rajifo
CC R
                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86
  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                   3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 LDEAMGSSEWLALTKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCCKWGCSKSEISS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 PGAEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAHEAMGDTFPDADADEDSLAGE 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40 MEEKM-----GFAKKCCAIGCSTEDFRM 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBGNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO DISULFIDE BONDS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEYDIG INSULIN-LIKE PEPTIDE B CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SUBCELLUTAR LOCATION: Secreted.
-1- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN LEYDIG CELLS.
-1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                             / Match 13.2%; Score 100.5; DB 1; Length 64; Local Similarity 22.1%; Pred. No. 0.002; nes 27; Conservative 11; Mismatches 25; Indels 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spiess A.-N., Pusch W., Ivell R.;
"Cloning and sequence of the rat relaxin-like factor and its
promotor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
LeCOT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Leydig insulin-like peptide (Ley-I-L) (Relaxin-like factor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: COULD PLAY A ROLE IN TESTICULAR FUNCTION AND SPERMATOGENESIS.
                                                                                                                                                                                                                       E7AC62B8BA81F49D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C PEPTIDE (POTENTIAL).
                                 RELAXIN B CHAIN.
                                                                                            RELAXIN A CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interpro: IPR00739; Insulin_IGF_relaxin.
Pfam: PF00049; Insulin; 1.
SWART; SM00078; IlGF; 1.
                                                                                                                          INTERCHAIN.
                                                                                                                                                               INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF139918; AAD33663.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00262; INSULIN; 1. Insulin family; Hormone.
                             40
41
64
51
64
55
7499 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Insulin family; Hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insulin family; H
NON_TER 1
CHAIN <1
PROPEP 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INSL3 OR RLF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 LC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 VC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Fragment)
                                                                                                                                                 DISULFID
                                                           NON_CONS
                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INL3_RAT
                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INL3_RAT
ET ET ES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HE WENT WAS A STREET OF THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
```

FT FT SO	•	CHAIN DISULFID DISULFID DISULFID SEQUENCE	80 6 18 89 105 AA;	105 90 103 94 11674 MW	LEYDIG INSULIN INTERCHAIN (BY INTERCHAIN (BY BY SIMILARITY. 7; 903716A8FBEB	05 LEYDIG INSULIN-LIKE PEPTIDE A CHAIN 90 INTERCHAIN (BY SIMILARITY). 03 INTERCHAIN (BY SIMILARITY). 94 BY SIMILARITY. 11674 MW; 903716A8FBEBI3EE CRC64;	PEPTIDE JARITY). JARITY).	а снаш	ż		
	Query M Best Lo Matches	atch cal Si	milarity Conserv	13.2%; 24.8%; ative 1	Query Match 13.2%; Score 100.5; DB Best Local Similarity 24.8%; Pred. No. 0.0035 Matches 35; Conservative 11; Mismatches	Query Match 13.2%; Score 100.5; DB 1; Length 105; Best Local Similarity 24.8%; Pred. No. 0.0035; Matches 35; Conservative 11; Mismatches 34; Indels 61	1; Length 1; ; 34; Indels	105;	Gaps	6;	
Οy		ARAAP	YGVRLCGRE	FIRAVIFT	GGSRWRRSDI	25 ARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAHEAMGDTFPDADADBDSLAGELDEA 84	DADADEDS	LAGELDI	EA 84		
qq	1	ARA	KLCGHH	LVRALVRV	GGPRWS	ARAPEATQPVDTRDREL	EATOPVDI	RDREL	38		
QY		MGSSE	WL	?	NLTKSP	85 MGSSEWLALTKSPQAFYRGRPSWQGTPGVLRGSRDVL 121	SWOGTPGV	TRGSRD	/L 121		
qa		LQ	WLEQRHLLH	IALVADADP?	NLDPDPALDP(39LQWLEQRHLLHALVADADPALDPDPALDPQLPHQASQRQR		RSVA 82	/A 82		
QΥ		AGLSS	SCCKWGCSKSEISSLC	122 AGLSSSCCKWGCSKSEISSLC 142	142						
qu		TNAVH	RCCLTGCTQ	83 TNAVHRCCLTGCTQQDLLGLC 103	103						
S, J	earch co	mplete 485 s	d: June 2 ec	Search completed: June 27, 2002, 16:16:51 Job time: 485 sec	16:16:51						

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

June 27, 2002, 16:08:09 ; Search time 73.16 Seconds

(without alignments) 36.438 Million cell updates/sec

US-09-781-077-2_COPY_119_142 Perfect score:

1 DVLAGLSSSCCKWGCSKSEISSLC 24 Sequence:

Gapop 10.0 , Gapext 0.5 Scoring table:

747574 seqs, 111073796 residues Searched:

747574 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

Database :

| SIDS1/gcddata/hold-geneseq/geneseqp-embl/Aa1983.DAT:*
| SIDS1/gcddata/hold-geneseq/geneseqp-embl/Aa1984.DAT:*
| SIDS1/gcddata/hold-geneseq/geneseqp-embl/Aa1986.DAT:*
| SIDS1/gcddata/hold-geneseq/geneseqp-embl/Aa1986.DAT:*
| SIDS1/gcddata/hold-geneseq/geneseqp-embl/Aa1986.DAT:*
| SIDS1/gcddata/hold-geneseq/geneseqp-embl/Aa1989.DAT:*
| SIDS1/gcddata/hold-geneseq/geneseqp-embl/Aa1989.DAT:*
| SIDS1/gcddata/hold-geneseq/geneseqp-embl/Aa1989.DAT:*
| SIDS1/gcddata/hold-geneseq/geneseqp-embl/Aa1989.DAT:*
| SIDS1/gcddata/hold-geneseq/geneseqp-embl/Aa1989.DAT:* /SIDBI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:
/SIDBI/gcgdata/hold-geneseq/geneseqp-embl/AA1992.DAT:
/SIDBI/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:
/SIDBI/gcgdata/hold-geneseq/geneseqp-embl/AA1994.DAT:
/SIDBI/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:
/SIDBI/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT: /SIDS1/gcgdata/hold-geneseg/genesegp-emb1/AA1996.DAT:*/SIDS1/gcgdata/hold-geneseg/genesegp-emb1/AA1997.DAT:* /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1998.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:* /SIDS1/gcgdata/hold-geneseq/geneseqp-embi/AA1982.DAT:* /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:* /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981. A_Geneseq_032802:* 10: 111: 12: 13: 14: 15: 16: 17: 17: 19: 20:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT

Description	Human insulin homo Mouse Insulin homo Mouse insulin fami Human relaxin-rela Human Zins2 testis-s Sequence encoded b Sequence of porcin Sequence of porcin Insulin-like pepti Human Zins3 protei
SUMMARIES	AAG78114 AAW37926 AAY925771 AAW17675 AAW47548 AAW47547 AAP30192 AAP30192 AAP40156 AAY01962 AAW37925
DB	22 119 119 119 119 119 119
% Query Match Length DB]	142 135 135 213 22 188 182 182 135
% Query Match	100.0 47.7 46.2 46.2 44.7 44.7 44.7 44.3 9.9 43.9 43.9
Score	132 633 63 61 61 59 58 58 58 57
Result No.	1 2 3 4 4 6 6 7 7 7 10 11

Pro-insulin-like p PRO182 polypeptide Human PRO182 prote Human insulin fami PRO182 Polypeptide Human EST encoded	Human immunostimul Human anglogenesis Rat RBK7 eph.relat Rat receptor tyros C. elegans insulin Mouse Bsk receptor	Human immune/haema Prorelaxin A-chain Relaxin analogue A Locust Lirp insuli Prolrelaxin fragme H2 prorelaxin gene	H2 prorelaxin dedu Sequence of human Amino acid sequenc Novel human diagno Drosophila melanog Propionibacterium Arabidopsis thalia	
AAY01961 AAB00173 AAB24391 AAY95770 AAY83228 AAM24033	AAB20110 AAB53072 AAR97853 AAW83147 AAY65654 AAW71628	AAR87941 AAM90349 AAR64896 AAW10304 AAB06162 AAR64904 AAR07987	AARVO 988 AAPVO 10 8 AAPVO 10 8 AAPVO 20 74 74 AABVO 813 4 AAGO 8134 AAGO 8133 AAGO 8133 AAGO 8133 AAGO 8133 AAGO 8133 AAGO 8133 AAGO 8133 AAGO 8133	
			221 221 221 221 221 221 221	
1322 1322 1322 1322 1322	135 135 928 1005 91 877	162 162 24 24 150 162	185 185 185 185 185 313 313 313 313 325 325	
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4			0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
557 557 558 578 578	557 57 58 58 58	5 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	51 51 51 51 51 51 51 51 51 51 51	
12 113 114 116	222 222 243 243	25 22 33 31 32		

ALIGNMENTS

antifertility; vasotropic; reproductive disorder; prostate disorder; heart disorder; kidney disorder; gonadal development; pregrancy; pubbertal change; menopeuse; ovarian cancer; testicular cancer; coulation; polycystic ovarian syndrome; contractile tissue; cardiovascular disease; birth control; impotence; myocyte; endothalial cell; osteoblast; blood pressure; muscle tension; osmotic balance; gene therapy. Human; insulin; zins4; relaxin; chromosome 19p13.11; cytostatic; /label= B_chain_consensus_sequence_region /note= "Given in SEQ ID NO 3" /label= mature_protein /note= "Zins4, claimed in claim 4" 37..41 /label= B_chain_conserved_motif 'note= "Claimed in claim 1" Human insulin homologue polypeptide Zins4. /label= signal_peptide 26..142 AAG78114 standard; Protein; 142 AA. Location/Qualifiers /label= B_chain (first entry) Homo sapiens. 21-NOV-2001 AAG78114; Peptide Protein Region Region Region RESULT

7

```
/note= "Cleavage site at the junction of the C peptide and the A chain with a conserved RXXR motif"
"Given in SEQ ID NO 5"
                                                       /label= A_chain
/note= "Claimed in claim 2"
                           "Claimed in claim 3"
                                                                                                                                                                                                      Claim 6; Page 72-73; 79pp; English.
                                                                                                                                               Holloway JL, Lok S, Jaspers SR;
                 /label - C_peptide
                                                                                                                         10-MAR-2000; 2000US-0523346.
                                                                                                              09-FEB-2001; 2001WO-US04199.
                                                                                                                                    (ZYMO ) ZYMOGENETICS INC.
                                                                  .142
                                 118
                                                  119..142
            ..118
 /note=
53..54
                            /note=
                                                                                                                                                           WPI; 2001-582454/65.
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 142 AA;
                                                                                                                                                                N-PSDB; AAH79088.
                                                                                          WO200168862-A1
                                  Cleavage-site
       Cleavage-site
                                                                                                     20-SEP-2001
                                                   Region
                                                                    Region
                        Region
             Region
```

```
The invention relates to an isolated insulin homologue zins4 having homology to the relaxin family. The zins4 gene, located on chromosome comprises a 142 amino acid protein, where the Zins4 polypeptide comprises a behain and A chain comprising amino acid residues 26-52 and comprises a behain and A chain comprising amino acid residues 26-52 and 19-142 respectively, joined by inter- and intra-chain disulfide bonds. The state of the selection in applications for enhancing fertilisation during assisted reproduction in humans and animals and in therapies for treating reproductive disorders. Intex4 protein is useful in treating reproductive, prostate, heart or kidney disorders and to identify cells, tissues or cell lines which respond to the zins4-stimulated pathway and to identify inhibitors of its activity. Zins4 polypeptides and modulators of the polypeptide are useful in treating disorders associated with gonadal collypeptide are useful in treating disorders associated with gonadal development, pregnancy, pubertal changes, menopause, ovarian cancer, prostate, testicular cancer, fertility, ovarian function, ovulation, propostic ovarian syndrome and other reproductive functions including pathological conditions in ovary. Detection of zins4 polypeptides in the serious prostate is as a patient is useful for diagnosing ovarian concerned the molecules are also useful for treating dysfunction associated with contractile tissues or to suppress or enhance contractility in vivo, that however the molecules are also useful in treating cardiovascular disease, infertility, in vitro fertilization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        birth control, treating impotence or other male reproductive dysfunction, inducing birth, for promoting growth, differentiation, development and/or maturation of ovarian cells, myocytes, endothelial cells, osteoblasts in culture and in the study of the ovarian cycle, reproductive function, ovarian cell-cell interactions and fertilisation. The polypeptide is also useful as a modulator of blood pressure, muscle tension and osmotic balance. The zins4 polynucleotide is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New insulin homologue polypeptide having homology to relaxin family, designated zins4 and zins4 polynucleotide, useful for diagnosing, preventing, treating reproductive, prostate, heart and kidney disorders
/label= A_chain_consensus_sequence_region
/note= "Given in SEQ ID NO 4"
```

ö

Gaps

ó;

h 100.0%; Score 132; DB 22; Length 142; Similarity 100.0%; Pred. No. 1.5e-09; 24; Conservative 0; Mismatches 0; Indels 0;

24;

Query Match Best Local S Matches

```
associated with the polypeptide, such as reproductive disorders associated with the placent and uterus, gastrointestinal diseases, and placental and colon pathology. Antagonists against the polypeptide may also be used to treat diseases such as preclampsia, premature labour, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Zins3 protein is an insulin homologue protein. Polynucleotide molecules taken from its gene can be introduced into a cultured cell using an expression vector. The cell will express an insulin homologue polypeptide encoded by the polynucleotide. The polypeptides can also be expressed by introducing the polynucleotides into the germline of a nonhuman animal. The polypeptides can be used to identify and isolate nonhuman animal. Antibodies and antagonists of the polypeptides can be used for treating disease associated with extracellular matrix and be used for treating disease associated with extracellular matrix and vessels. The antibodies may also be used in the diagnosis of diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insulin homologue polypeptide(s) and antagonists – used to, e.g. treat pre-eclampsia, premature labour and Crohn's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                               Insulin homologue; identification; isolation; Zins3 receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.7%; Score 63; DB 19; Length 135; 52.6%; Pred. No. 0.88; tive 4; Mismatches 5; Indels
                                                                                                                                                                                                                                            treatment; disease; pre-elampsia; premature labour; Human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lok S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conklin DC, Jaspers SR, Lofton-Day CE,
                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                          49..115
/note= "C-peptide"
116..135
                                                                                                       AAW37926 standard; Protein; 135 AA.
                /note= "A chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 9; Page 67; 81pp; English.
                                                                                                                                                                                                                                                                                                                                             /note= "B chain"
1 DVLAGLSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97WO-US18593.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96US-0028177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 52.6%
Matches 10; Conservative
                                                                                                                                                                        01-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-251285/22.
                                                                                                                                                                                                       Mouse Zins3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAV29153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Crohn's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9816635-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-APR-1998.
                                                                                                                                           AAW37926;
                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                      Mus sp.
                                                                                 RESULT
                                                                                                                                           δλ
                               qq
```

117 lqalccregcsmkelstlc 135

QQ

```
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is that of a murine paralog (see AAY95771) of funnan 21ns3 (see AAY95770), a novel member of the insulin/relaxin family member that maps to a region of human chromosome 1 associated with non-insulin dependent diabetes mellitus (NIDDM). The sequence blots of embryo tissue indicated that mouse zins3 is expressed in a developmentally regulated fashion. Zins3 polynucleotides and a developmentally regulated fashion. Zins3 polynucleotides and abnormal expression of zins3, and to identify polynorphisms that result from mutations in the human zins3 gene. The invention considered a factor in causing, or predisposing, a person to some defect in glucose metabolism, such as NIDDM.
                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying mutations in human chromosome 1p31, preferably a zins3 gene mutation, comprises using an insulin/relaxin family member (designated zins3), useful for diagnosing non-insulin dependent diabetes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                            Lok S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47.7%; Score 63; DB 21; Length 135; 52.6%; Pred. No. 0.88;
                                                                                                                                                                                                                                                                                                                                                          Jaspers SR, Whitmore TE, Conklin DC, Lofton-Day CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Indels
                                                                                                                                    Zins3; insulin; relaxin; mouse; NIDDM;
non-insulin dependent diabetes mellitus; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                           Mouse insulin family homologue zins3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; Page 46-47; 51pp; English.
                       AAY95771 standard; Protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW17675 standard; Protein; 213 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4;
                                                                                                                                                                                                                                                            10-FEB-2000; 2000WO-US03515,
                                                                                                                                                                                                                                                                                            99US-0198248.
99US-0250125.
                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | : ||: ||| |:|:||
117 |qalccregcsmkelstlc 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                  (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-JUL-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 52.69
Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-558220/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAA50153,
                                                                                                                                                                                                         WO200047776-A2.
                                                                                                                                                                                 Mus musculus.
                                                                                                                                                                                                                                                                                         12-FEB-1999;
12-FEB-1999;
                                                                               07-NOV-2000
                                                                                                                                                                                                                                  17-AUG-2000.
                                                     AAY95771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW17675;
RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW17675
                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   XXAC
```

```
New isolated relaxin related factor genes - used to develop products which can be used in diagnosis and therapy, e.g. in fertility and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human relaxin-related factor-1 (RRF-1) (AAW17675) is a testis-specific growth factor related to relaxin and to the insulin family of ligands. RRF-1 cDNA (AAY68418) was isolated in a search of displays all the expected features of a new insulin family member, expressed sequence tags for sequences related to relaxin. RRF-1 partic. with regard to a cluster of four cysteine residues at the Terminus of the molecule. A related placenta specific factor, in transformed host calls for use in the prepn. of antiboodies and the representation of a sequence of a sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in culture. RRF-1 may be involved in the maturation of sperm and may have a role in treatment of fertility disorders.
                                                                     Relaxin-related factor-1; RRF-1; testis; sperm; growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                                                                                            /note= "conserved Cys residue indicative of
                                                                                                                                                                                                                                                                                                                                                                 /note= "conserved Cys residue indicative of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "conserved Cys residue indicative of insulin family member"
                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "conserved Cys residue indicative of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.2%; Score 61; DB 18; Length 213;
50.0%; Pred. No. 2.4;
tive 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                        insulin family member"
                                                                                                                                                                                                                                                                                                                                                                                                insulin family member"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  insulin family member"
                    Human relaxin-related factor-1 (RRF-1).
                                                                                                                                                                                                                                         label Sig_peptide
                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Fig 1; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96WO-US17342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-0006221.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96US-0012016.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (REGE-) REGENERON PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 GLSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 50.09
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 192
/note=
                                                                                                                                                                                                                                                                                                                                  Misc-difference 179
                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-272118/24.
                                                                                                                                                                                                                                                                Misc-difference 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    213 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAT68418.
                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9716549-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-MAY-1997
                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Davis S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
ò
```

173 gysekccltgctkeelsiac 192

RESULT AAW47548

```
Stewart AG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JAN-1983
          Rattus rattus
                                                                                                                           21-NOV-1996;
                                     WO9805782-A1.
                                                                                             01-AUG-1997;
                                                                                                                                        02-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP68375-A.
                                                                 12-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAP30192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      restis-specific insulin homologue poly:peptide(s) - may be used, e.g. in enhancing viability of cryo:preserved sperm, enhancing sperm motility or in immuno:contraception methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is human ZinsZ testis-specific insulin homologue, which may be used to enhance the viability of cryopreserved sperm, sperm motility, egg/sperm interactions, fertilisation or proliferation or differentiation of testicular immunocontraception methods to prevent fertilisation. Antagonists, e.g. anti-ZinsZ binding protein, may be used in contraception. ZinsZ is especially useful for in vitro fertilisation methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat; Zins2; testis-specific insulin homologue; differentiation; cryopreserved sperm viability; sperm motility; proliferation; egg/sperm interaction; fertilisation; testicular cell; vaccine; immunocontraception; contraception; in vitro fertilisation.
                                                                                                                                                                                                                                                                                                                                                                                    Conklin DC, Jaspers SR, Jelmberg AC, Lofton-Day CE;
                                                                                                                Human, Zins2; testis-specific insulin homologue; differentiation; cryopreserved sperm viability; sperm motility; prolliferation; egy/sperm interaction; fertilisation; testicular cell; vaccine; immunocontraception; contraception; in vitro fertilisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.2%; Score 61; DB 19; Length 213; 50.0%; Pred. No. 2.4; tive 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat Zins2 testis-specific insulin homologue.
                                                                                            Human Zins2 testis-specific insulin homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 10; Pages 73-74; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW47547 standard; Protein; 188 AA.
         AAW47548 standard; Protein; 213 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 gysekccltgctkeelsiac 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 GLSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                           97WO-US13879.
                                                                                                                                                                                                                                                                                                                                     96US-0023213.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                       96US-0031592.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 50.07
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                (ZYMO ) ZYMOGENETICS INC.
                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-145618/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAV18663
                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                           01-AUG-1997;
                                                                                                                                                                                                                                    WO9805782-A1
                                                                                                                                                                                                                                                                                                                         21-NOV-1996;
                                                                                                                                                                                                                                                                                                                                        02-AUG-1996;
                                                                         03-JUL-1998
                                                                                                                                                                                                                                                               12-FEB-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW47547;
                                                                                                                                                                                                                                                                                                                                                                                                  Adams RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                           AAW47548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
AAW47547
```

g

οy

```
Gaps
                                                                                                                                                                                                                                                                                         Testis-specific insulin homologue poly:peptide(s) - may be used, e.g. in enhancing vlability of cryo:preserved sperm, enhancing sperm motility or in immuno:contraception methods
                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is rat Zins2 testis-specific insulin homologue, which may be used to enhance the viability of cryopreserved sperm, sperm motility, egg/sperm interactions, fertilisation or proliferation or differentiation of testicular immunocontraception methods to prevent fertilisation. Antagonists, e.g. anti-Zins2 binding protein, may be used in contraception. Zins2 is especially useful for in vitro fertilisation methods.
                                                                                                                                                 Adams RL, Conklin DC, Jaspers SR, Jelmberg AC, Lofton-Day CE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence encoded by synthetic gene for porcine relaxin A chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hormone; labour; pregnancy; parturition; control; induction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.7%; Score 59; DB 19; Length 188;
45.0%; Pred. No. 3.8;
tive 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; Pages 66-67; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAP30192 standard; Protein; 22 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | : || |||| |: |
163 gfadkccaigcskeelavac 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81GB-0019138.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 GLSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82EP-0105405
                                                                   96US-0023213.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-AUG-1992 (first entry)
97WO-US13879.
                                               96US-0031592.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SEAR ) SEARLE G D & CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                   (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bell LD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                         WPI; 1998-145618/13.
                                                                                                                                                                                                                                                                N-PSDB; AAV18662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUN-1982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-JUN-1981;
```

ö

182 AA;

Seguence

g

ö

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The inventors claim synthetic porcine preprorelaxin and prorelaxin and synthetic A, B and C peptide chains of prolaxin, and a gene for expression of porcine preprorelaxin or prorelaxin, and their subunits (see AAN30186). They also claim a double-stranded DNA fragment for the expression of the signal peptide chain of porcine preprorelaxin comprising a coding strand and a complementary strand corresp. to a defined mRNA sequence (see AAN30187-N30194) which corresp. to the most homologous regions between the pig and rat cDNA sequences. A probe (AAN30195) is also claimed.
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                           The genes
                                                                                                                The inventors claim synthetic genes for porcine relaxin. The genes may contain, in addn to the coding sequence, a stop codon, an initiator methionine codon, restriction sites for Cla I and Bam HI etc. Porcine relaxin is useful in the induction and control of labour in women. In sows admin. during farrowing may reduce the rate of still birth of piglets.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genes and DNA transfer vectors for prorelaxin expression - useful
in prodm. of porcine relaxin for veterinary and human use
                                                                                                                                                                                                                                                                                                         ;
0
                                          Prodn. of porcine relaxin from synthetic genes - useful for induction and control of labour in women
                                                                                                                                                                                                                                                                  43.9%; Score 58; DB 4; Length 22;
47.4%; Pred. No. 0.74;
tive 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shine J;
                                                                                                                                                                                                                                                                                                                                                                                                                             AAP30392 standard; Protein; 182 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence of porcine preprorelaxin.
                                                                                     Disclosure; Fig 1; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 5; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Niall HD,
                                                                                                                                                                                                                                                                                                                         6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                             4 lsekccqvgcirkdiarlc 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83EP-0021967.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82AU-0002695.
83AU-0011834.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (FLOR-) FLOREY INST EXP PHY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HOWA-) HOWARD FLOREY INST
                                                                                                                                                                                                                                                                                               9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hudson PJ, Haley JD,
WPI; 1983-04897K/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sus scrofa domestica,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1983-748587/35.
                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                          22 AA;
               N-PSDB; AAN30124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Relaxin; hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAN30196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-FEB-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-FEB-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-FEB-1982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 - AUG - 1983.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP86649-A.
                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAP30392;
                                                                                                                                                                                                                                                                  Query Match
ò
                                                                                                                                                                                                                                                                                                                                                    g
```

```
ö
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       are prepd. for therapeutic purposes, esp. in clinical intervention in cases of difficult labour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The inventors claim the gene for the expression of human preprorelaxin (HPP) and its sub-units. Also claimed are synthetic HPP, HP, fragments and analogues. Human relaxin and its analogues
                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genes for human relaxin, prorelaxin and preprorelaxin prodn. prepd. by recombinant DNA techniques
             DB 4; Length 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 58; DB 5; Length 182;
Pred. No. 5;
4; Mismatches 6; Indels
                                  6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hudson PJ, Shine J, Niall HD, Tregear GW;
                                4; Mismatches
            43.9%; Score 58; 47.4%; Pred. No.
                                                                                                                        AAP40156 standard; Protein; 182 AA.
                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                       Sequence of porcine preprorelaxin.
                                                                                                                                                                                                                                                                                                                   /label= C-peptide
                                                                                                                                                                                                           Labour; birth; hormone; relaxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 3; 51pp; English.
                                                                                                                                                                                                                                                                                     26..57
/label- B-chain
                                                                                                                                                                                                                                                                                                                                       /label= A-chain
                                                                                                                                                                                                                                                                           'label= signal
                                                                164 lsekccqvgcirkdiarlc 182
                                                  6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                     83EP-0304662.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                              88EP-0104503
                                                                                                                                                                                                                                                                                                                                                                                                                                    83AU-0017906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAN40125, AAN40126.
                                                                                                                                                                  11-FEB-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (FLOR-) HOWARD FLOREY INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HOWA-) HOWARD FLOREY INST.
                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 47.49
Matches 9; Conservative
Query Match
Best Local Similarity
9, Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1984-050918/09
                                                                                                                                                                                                                                                                                                                                                                                                    11-AUG-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                        12-AUG-1982;
                                                                                                                                                                                                                                                                                                                                                          EP101309-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       are prepd.
                                                                                                                                              AAP40156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                Pig.
                                                                                                                                             ŏ
```

6 LSSSCCKWGCSKSEISSLC 24

ò

AAY01962 RESULT

g

```
AAW37925;
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents insulin-like polypeptide (pro-ILP) chain A peptide. The ILP protein is expressed in the colon and uterus, and is a member of the insulin/TGF family. The immature pro-ILP comprises a 135 amino acid sequence, which is processed into the mature form which comprises an A chain and a B chain linked by disulfide bonds. The CPEPtide of pro-ILP syststs as a separate peptide after processing of pro-ILP. The ILP protein is useful in treatment of disorders related to meurophysiological function affecting fluid homeostasis, electrolyte concestasis, cardiovascular function, blood pressure, somatic or cardiac innortopic activity, cardiac chronitopic activity and collagen concessing pathologic condition of the uterus, colon or other ILP-expressing cell pathologic condition of the uterus, colon or other ILP-expressing cell content the present sequence does not appear in the specification; it was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                Insulin-like polypeptide; pro-ILP; ILP; insulin/IGF family; A chain; B chain; C chain; neurophysiological function; fluid homeostasis; electrolyte homeostasis; cardiovascular function; blood pressure; somatic; cardiac innotropic activity; cardiac chronotropic activity; collagen deposition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Colon and uterus expressed insulin-like polypeptide, useful in the treatment of disorders related to neurophysiological function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.2%; Score 57; DB 20; Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Indels
                                                                                                                                                                                                          Insulin-like peptide (pro-ILP) chain A peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW37925 standard; Protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            created using information provided.
                                                                                                       AAY01962 standard; Peptide; 27 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; Page -; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | : || ||| :::|:||
9 lqtlcctdgcsmtdlsalc 27
          98WO-US17888.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-0059836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 47.4
Matches 9; Conservative
                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-254713/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAX35209
                                                                                                                                                                                                                                                                                                                                                                               WO9915664-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-SEP-1997;
                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                28-AUG-1998;
                                                                                                                                                                            01-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gurney A;
                                                                                                                                          AAY01962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
```

```
associated with the polypeptide, such as reproductive disorders associated with the polypeptide, such as reproductive disorders associated with the placente and uterus, gastrointestinal diseases, and placental and colon pathology. Antagonists against the polypeptide may also be used to treat diseases such as preclampsia, premature labour, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              molecules taken from its gener can be introduced into a cultured cell using an expression vector. The cell will express an insulin homologue bolypeeptide encoded by the polymucleotide. The polypeptides can also be expressed by introducting the polymucleotides into the germine of a nonhuman animal. The polypeptides can be used to identify and isolate receptors for zins3. Antibodies and antagonists of the polypeptides can be used for treating disease associated with extracellular matrix and vessels. The antibodies may also be used in the diagnosis of diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Insulin homologue polypeptide(s) and antagonists - used to, e.g. treat pre-eclampsia, premature labour and Crohn's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                         Insulin homologue; identification; isolation; Zins3 receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.2%; Score 57; DB 19; Length 135;
47.4%; Pred. No. 5.1;
tive 5; Mismatches 5; Indels
                                                                                                                    treatment; disease; pre-elampsia; premature labour; Human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Zins3 protein is an insulin homologue protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lok S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lofton-Day CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY01961 standard; Protein; 135 AA.
                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Page 64-65; 81pp; English.
                                                                                                                                                                                                                                                                                                                                "C-peptide"
                                                                                                                                                                                                                                                                                  "B chain"
                                                                                                                                                                                                                                                                                                                                                                                    /note= "A chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 lqtlcctdgcsmtdlsalc 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97WO-US18593.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96US-0028177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 47...
Best Local 9; Conservative
01-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                /note= "C
115..135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conklin DC, Jaspers SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ZYMO) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                           .114
                                                                                                                                                                                                                                                          23..48
/note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-251285/22.
N-PSDB; AAV29150.
                                                   Human Zins3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Crohn's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-OCT-1996;
                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                          W09816635-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-APR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY 01961;
                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY01961
```

ö

AAW37925

qq δy

01-JUL-1999 (first entry)

human.

```
The present sequence represents an insulin-like polypeptide (pro-ILP). The protein is expressed in the colon and uterus, and is a member of the insulin/IGF family. The immature pro-ILP comprises a 135 amino acid sequence, which is processed into the mature form which comprises pro-ILP exists as a separate peptide after processing of pro-ILP. The neurophysiological function affecting fluid homeostasis, electrolyte homeostasis, cardiovascular function, blood pressure, somatic or cardiac indictopic activity, cardiac chrontople activity and collagen deposition. The methods can be used for diagnosing a physiologic or pathologic condition of the uterus, colon or other ILP-expressing cell or tissue and for diagnosis and therapeutics.
                                                                                                                                                           Insulin-like polypeptide; pro-ILP; ILP; insulin/IGF family; A chain; B chain; C chain; neurophysiological function; fluid homeostasis; electrolyte homeostasis; cardiovascular function; blood pressure; somatic; cardiac ionotropic activity; cardiac chronotropic activity; collagen deposition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Colon and uterus expressed insulin-like polypeptide, useful in the treatment of disorders related to neurophysiological function
                                                                                  Pro-insulin-like peptide (pro-ILP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; Fig 6B; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98WO-US17888.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0059836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-254713/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAX35204.
                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9915664-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gurney A;
HANDER WANTER WA
```

```
Gaps
                                                                                                                                                                                                                                                                                                                           tumour; treatment; therapy; agonist; antibody; breast cancer; ovarian cancer; renal cancer; colorectal cancer; uterine cancer; prostate cancer; lung cancer; bladder cancer; melanoma; leukaemia; inflammatory disorder; angiogenic disorder; immunologic disorder;
                                                       ;
                                                                                                                                                                                                                                                                                                            PRO211; PRO228; PRO538; PRO172; PRO182; neoplasia; inhibition;
                   43.2%; Score 57; DB 20; Length 135;
47.4%; Pred. No. 5.1;
tive 5; Mismatches 5; Indels
                                                                                                                                                                                       AAB00173 standard; Protein; 135 AA.
                                                                                                   Ouery Match
Best Local Similarity 47.4%;
Chas 9, Conservative
                                                                              6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                08-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                 PRO182 polypeptide.
                                                                                                                                                                                                                    AAB00173;
                                                                                                                                                          13
                                                                                                                                                                         AAB00173
                                                                                                                                                        RESULT
                                                                              ŏ
                                                                                                         g
                                                                                                                                                                                                    XX
AC
XX
XX
DE
XX
XX
XX
XX
XX
XX
XX
```

```
"cAMP- and cGMP-dependent protein kinase
                                                                       "Casein kinase II phosphorylation site"
                                                                                                          "Casein kinase II phosphorylation site"
                                                                                                                                              /note= "Casein kinase II phosphorylation site"
                                                                                                                       Insulin family signature
                                               /note= "N-myristoylation site"
                                                           "N-myristoylation site"
                                                                            96.102
/note= "N-myristoylation site"
                                                                                                                                   'note= "N-myristoylation site"
                               1..18
∕label≈ Signal peptide
                        Location/Qualifiers
                                                                                                                                                                                   99WO-US28564.
                                                                                                                                                                                               99US-0123957
                                                                                                                                                                                                          99US-0144758.
                                                                                                                                                                                                                            99WO-US21090.
                                                                                                                                                                                                                       99WO-US20594
                                                                                                                                                                                                                                         99WO-US28313
                                                                                                                .136
                                                                                         ..111
                                                                                                     .117
                                                                                                                             125..131
                                                                                                                                          ..131
                                                                                                                       /label=
                                                            /note=
88..92
                                                                                                /note=
                                                                        'note=
                                                                                                           /note=
                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC.
                                                                                                                                                          WO200055319-A1.
                                                     Modified-site
                                                                Modified-site
                                         Modified-site
                                                                                        Modified-site
                                                                                                   Modified-site
                                                                                                                                       Modified-site
            Homo sapiens.
                                                                                                                            Modified-site
                                                                                                                                                                                   02-DEC-1999;
                                                                                                                                                                      21-SEP-2000
                                                                                                                                                                                                                            15-SEP-1999;
                                                                                                                                                                                                                                        30-NOV-1999;
                                                                                                                                                                                                    28-APR-1999
                                                                                                                                                                                                                26-JUL-1999
                                                                                                                                                                                                                       08-SEP-1999
                                                                                                                                                                                                                                  05-0CT-1999
                             Peptide
```

Ashkenazi AJ, Goddard A, Gurney AL, Klein RD, Napier MA, Wood WI; PRO211, PRO228, PRO538, PRO172 and PRO182 polypeptides useful for treating tumors including cancers of the breast and lung, leukeamia and for identifying compounds capable of inhibiting WPI; 2000-638201/61. N-PSDB; AAA54109 Yuan J;

Claim 31; Fig 10; 133pp; English. growth of neoplastic cells

Isolated PRO211, PRO228, PRO538, PRO172 or PRO182 polypeptides

Cor their agonists (preferably anti-PRO agonist antibody or a small
molecule minicking the biological activity of PRO polypeptide) are
useful in vitro or in vivo for inhibiting the growth of a tumour cell.
Compositions comprising the PRO polypeptides are useful for
inhibiting neoplastic cell growth and for treating cancer including
breast, ovarian, renal, colorectal, uterine, prostate, lung, bladder,
central nervous system cancer, melanoma and leukemia in a mammal.
The PRO polypeptides are also useful for treating other disorders
central nervous, gill, astrocytal, hypothalamic and other glandular,
and neuronal, gilal, astrocytal, hypothalamic and other glandular,
inflammatory, anglogenic and immunologic disorders and
inflammatory, anglogenic and immunologic disorders as well as being
cosful for identifying agonists to PRO polypeptides by contacting the
colypeptide with a candidate molecule and monitoring biological

135 AA; Sequence

ò g

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation; diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy; angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic; cytostatic; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorder in mammals by modulating cell proliferation, anglogenesis and cardiovascularisation, and for identifying agonists and antagonists of these processes. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goddard A;
                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or anglogenic disorders in mammals -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gerber H, Hillan KJ, Goddi
Kuo SS, Paoni NF, Smith V;
                                                  ö
                                                                                                                                                                                                                                     •
Score 57; DB 21; Length 135; Pred. No. 5.1; 5; Mismatches 5; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                   Human PRO182 protein sequence SEQ ID NO:16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baker KP, Ferrara N, Surney AL, Klein RD, FWilliams PM, Wood WI;
                                                                                                                                                                                                                                                             AAB24391 standard; Protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 72; Fig 8; 315pp; English.
       43.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US20111.
                                                                                                                           | : || ||| :::|:||
| 117 lqtlcctdgcsmtdlsalc 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US12252.
99US-0141037.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US20944.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US28313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US05028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0131445.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0144758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0145698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US20594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US21547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US23089.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0123957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0134287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Godowski PJ, Gurney AL, K
Watanabe CK, Williams PM,
                                                                                                     6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                       07-NOV-2000 (first entry)
            Query Match
Best Local Similarity 47.4'
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-412154/35.
N-PSDB; AAA77521.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200032221-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ashkenazi AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-JUN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-0CT-1999
                                                                                                                                                                                                                                                                                                              AAB24391;
                                                                                                                                                                                                                       14
                                                                                                                                                                                                                                             AAB24391
                                                                                                                                                                                                                       RESULT
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying mutations in human chromosome 1p31, preferably a zins3 gene mutation, comprises using an insulin/relaxin family member (designated zins3), useful for diagnosing non-insulin dependent diabetes
nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PRO expression such as cardiovascular, endothelial or angiogenic disorders in mammals (e.g. atherosolerosis, cancers and cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors containing them and the PRO polypeptide may be used to treat disorders associated with decreased PRO expression. AAA77510 to AAAA7721 and AAB24388 to AAB24435 represent nucleotide and protein sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is that of zins3, a novel member of the insulin/relaxin family. The zins3 gene maps to human chromosome 1p31, a region that is correlated to a heritable form of non-insulin dependent diabetes mellitus (NIDDM). zins3 mRNA is not expressed
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ľδ
                                                                                                                                                                                             43.2%; Score 57; DB 21; Length 135; 47.4%; Pred. No. 5.1;
                                                                                                                                                                                                                            5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conklin DC, Lofton-Day CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zins3; insulin; relaxin; human; diagnosis; NIIDM; non-insulin dependent diabetes mellitus.
                                                                                                                                                                                                                             5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human insulin family homologue zins3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 44-45; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                              AAY95770 standard; Protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= C-chain
115..135
/label= A-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23..48
/label= B-chain
                                                                                                                                                                                                                                                                             10-FEB-2000; 2000WO-US03515.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0250125,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0198248
                                                                                                                                                                                                                                                           6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jaspers SR, Whitmore TE,
                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                     Query Match
Best Local Similarity 47.4%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-558220/51.
N-PSDB; AAA50150.
                                                                                                                                                         135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200047776-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                       07-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-AUG-2000.
                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                           AAY95770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                   15
                                                                                                                                                                                                                                                                                                                                                 AAY95770
                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
             8.86666666688
```

in detectable amnounts in healthy tissue, indicating that the zins3

Specialized cell type. zins3 polynucleotides and polypeptides can
be used to diagnose disorders associated with abnormal expression

of the zins3 protein, and to identify polymorphisms that result

from mutations in the zins3 gene. In particular, the invention

provides methods for identifying abnormalities in expression that

are a factor in causing, or predisposing, a person to some defect

in glucose metabolism, such as NIDDM. Processing of the mature

c zins3 protein involves cleavage at the C-terminus of the signal

peptide and, based on predicted structural homology with other

members of the insulin family, cleavage at the C-terminus of the

B-chain and at the N-terminus of the A-chain, resulting in
removal of the C-peptide. Cysteine residues at positions 29 and 41

(B-chain) and 121 and 135 (A-chain) are capable of associating

through cysteine bridges and forming disulfide-bonded molecules. \$5555555555555555x 8

135 AA; Sequence

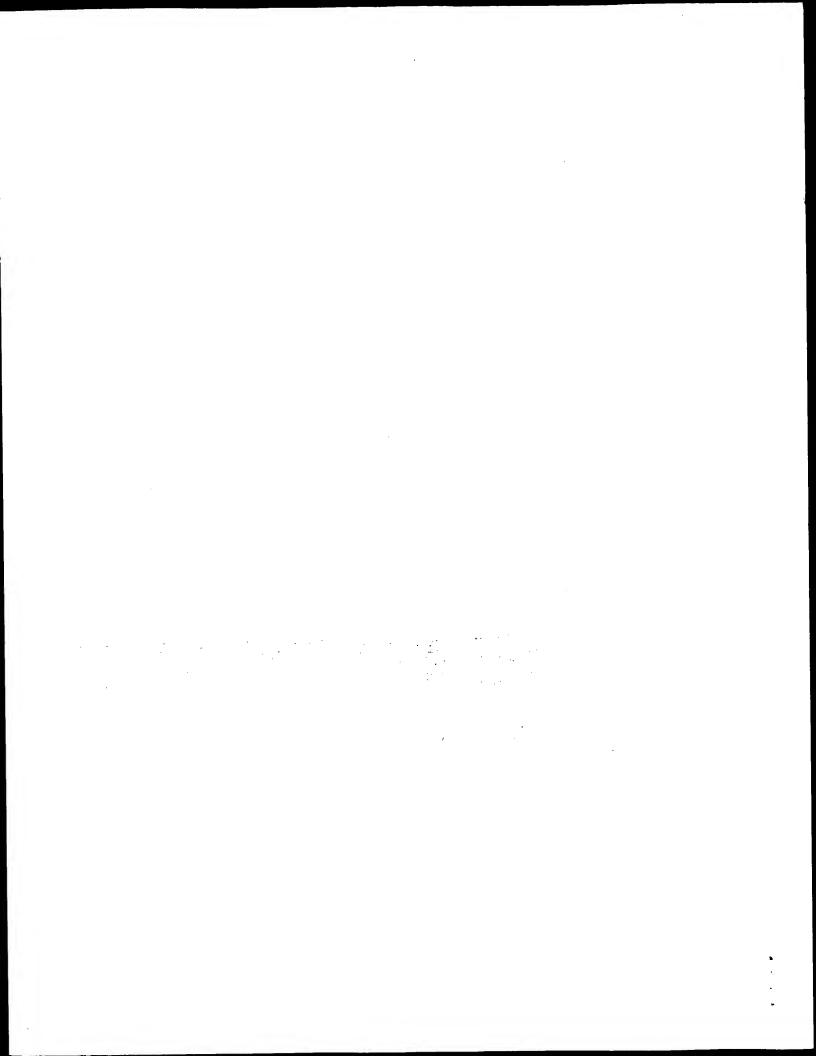
ö Gaps ; 0 Query Match

43.2%; Score 57; DB 21; Length 135;
Best Local Similarity 47.4%; Pred. No. 5.1;
Matches 9; Conservative 5; Mismatches 5; Indels

6 LSSSCCKWGCSKSEISSLC 24 ð

117 lqtlcctdgcsmtdlsalc 135 q

Search completed: June 27, 2002, 16:08:09 Job time: 278 sec



```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein . protein search, using sw model

June 27, 2002, 16:08:44; Search time 28.78 Seconds (without alignments) 20.369 Million cell updates/sec Run on:

US-09-781-077-2_COPY_119_142 Title: Perfect score:

1 DVLAGLSSSCCKWGCSKSEISSLC 24 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

231628 seqs, 24425594 residues Searched:

231628 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued_Patents_AA:*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/pcTuS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution:

SUMMARIES

		Description	!	Datont No. 5464/36	. O	0 -	7 :	٦ (vi c	7 P. C.	Patent No. 5464/56		7 (7	7		Sequence 103, App		Sequence 2 Appli) A	Segmence 2 April:	i c	, c	٧.	Sednence 4, Appli		Sequence 10, Appl	Sequence 10. Appl	12	1	Patent No. 5464756
		ΠD	5464756-8	5464756-7	US-08-950-720A-6	-905-267-	TIS-09-314-051+13	IIS-08-905-257-2		1	5464756-5	US-08-950-720A-2	TIS-08-440-048-0	118-08-440-815-2	Z-CT0 0## 00 G0	7-644	US-U8-469-53/A-103	5464756-1	US-08-673-789-2	US-08-443-568B-4	US-08-483-476-2	US-08-484-219-2	US-09-158-706-2	PCT-11S94-06997-A		2-06/4040	US-U8-443-568B-10	PCT-US94-06997-10	US-08-443-568B-12	PCT-US94-06997-12	5464756-18
		DB	9	9	m	n	4	٠ ٥	4	9	9	m	-	í -	۱ ح	, (١,	۰	~	-	7	7	4	Ŋ	· (c	٦ ٦	- 1	n	_	2	9
		Length	24	24	135	213	213	188	188	22	24	135	928	928	928	1000	700	47	877	24	24	24	24	24	24	11	- 1	//	150	150	162
dР	Query	Match	56.1	47.7	47.7	46.2	46.2	44.7	44.7	43.9	43.2	43.2	43.2	43.2	43.2		1 (4.6	41./	39.4	39.4	39.4	39.4	39.4	39.4	. 08		4.0	39.4	39.4	39.4
		score	74	63	63	61	61	59	59	28	57	57	57	57	57	57	יינ) L	0 1	52	25	25	52	52	52	יני	100	7 (70	25	25
	Result	NO.	н	7	m	4	Ŋ	9	7	80	6	10	11	12	13	14	15	1.	0 F	77	ю. Т	19	20	21	22	23	200	* "	0.7	56	27

ó

0; Gaps

Query Match
47.7%; Score 63; DB 6; Length 24;
Best Local Similarity 52.6%; Pred. No. 0.029;
Matches 10; Conservative 4; Mismatches 5; Indels

Patent No. 5464756 Sequence 12, Appl Sequence 89, Appl Patent No. 5464756 Sequence 91, Appl Sequence 2, Appl Sequence 4, Appl Sequence 4, Appl Sequence 6, Appl Sequence 7, Appl Sequence 7, Appl Sequence 7, Appl Sequence 7, Appl Sequence 35, Appl Sequence 35, Appl Sequence 35, Appl Sequence 32, Appl	; WILKINS, THE	Length 24; ; Indels 0; Gaps 0;	L.;WILKINS, OR THE
164 6 5464756-20 185 3 US-08-550-720A-12 24 2 US-08-533-476-89 25 6 546476-6 421 2 US-08-353-476-91 134 4 US-08-353-476-91 134 4 US-08-254-34 457 1 US-08-254-34 457 5 PCT-US95-07295-6 735 2 US-08-65-243-6 735 1 US-08-75-243-6 735 2 US-08-507-124-4 73 2 US-08-507-124-4 73 1 US-08-507-124-4 74 US-08-905-223-328 74 US-08-905-223-328	ALIGNMENTS BENNIS J.; VANDLEN, RICHARD L.; WILKINS L. G. PROCESS AND COMPOSITIONS FOR THE IN 42 DATA: " US/07/908,766 II-1992 III-1992 R. 347,550 R. 347,550 IY-1989	%; Score 74; DB 6; %; Pred. No. 0.0011; 5; Mismatches 4 24	NNIS J.; VANDLEN, RICHARD S. ROCESS AND COMPOSITIONS F 42 ATA: US/07/908,766 11992 A: 347,550
28 52 39.4 39.4 39.4 49.9 37.1 33.0 49.9 37.1 33.0 49.9 37.1 39.4 49.9 37.1 39.4 49.9 37.1 39.4 49.9 47.5 36.0 39.4 49.0 40.0 40.0 40.0 40.0 40.0 40.0 4	RESULT 1 5464756-8 ; Patent No. 5464756 ; JAMES A.; YANDLE, G.; JAMES A.; YANDLE, G.; TITLE OF INVENTION: PROCESS AND COMI ; ISOLATION HUMAN RELAXIN ; ISOLATION HUMAN RELAXIN ; WUMBER OF SEQUENCES: 42 ; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/O7/908,756 ; FILING DATE: 01-JUL-1992 ; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: 347,550 ; SEQ IF NILNG DATE: 04-MAY-1989 ; SEQ IF NILNG DATE: 04-MAY-1989 ; LENGTH: 24 5464756-8	Query Match Best Local Similarity 55.0 Matches 11; Conservative Qy 5 GLSSCCKWGGSKSEISSLC	RESULT 2 5464756 ; Patent No. 5464756 ; Patent No. 5464756 ; JAMES A.:YANSURA, DANIEL G. TITLE OF INVENTION: PROCESS AND COMPOSITION HUMAN RELAXIN ; NUMBER OF SEQUENCES: 42 ; CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/908,766 ; FILING DATE: 01-JUL-1992 ; RENOR APPLICATION DATA: RILING DATE: 01-JUL-1992 ; FRICH APPLICATION DATA: RILING DATE: 04-MAY-1989 ; SEQ ID NO:7: LENGTH: 24

```
ADDRESSEE: ZymoGenetics, Inc. STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/314,051
                                                              ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A.
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 96-06
TELECOMMUNCATION INFORMATION:
TELEPRAY: 206-442-6672
TELEFAX: 206-442-6678
                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173 GYSEKCCLTGCTKEELSIAC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 GLSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 213 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 213 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: protein US-08-905-267-13
                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 120-
TTY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98102
                                                                                                                                                                 98102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
US-09-314-051-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47.7%; Score 63; DB 3; Length 135; 52.6%; Pred. No. 0.15; tive 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/950,720A
                                                                                                                          Sequence 6, Application US/08950720A; Patent No. 6046028; GENRRAL INFORMATION:
APPLICANT: Conflin, Darrell C.
APPLICANT: Lofton-Day, Catherine E.
APPLICANT: Lok, Si
APPLICANT: Lok, Si
APPLICANT: Lok, Si
APPLICANT: Jaspers, Stephen R.
TITLE OF INVENTION: INSULIN HOWOLOG
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13, Application US/08905267; Patent No. 5989075; GENERAL INFORMATION:
APPLICANT: LOK, Si
APPLICANT: CONKlin, Darrell C.
APPLICANT: Adams, Robyn L.
APPLICANT: Jelmberg, Anna C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATORNEY/AGENT INFORMATION:
NAME: Savislak, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 96-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 LQALCCREGCSMKELSTLC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
6 LSSSCCKWGCSKSEISSLC 24
                      6 MSIKCCIYGCTKKDISVLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 47.7%
Best Local Similarity 52.6%
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein; FRAGMENT TYPE: internal US-08-950-720A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                            Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  98102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 4
US-08-905-267-13
                                                                                                                                                                                                                                                                                                                                                                                                 STATE: WA
                                                                                                                      US-08-950-720A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δλ
```

```
0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13, Application US/09314051
Patent No. 618391
GENERAL INFORMATION:
APPLICANT: LOK, Darrell C.
APPLICANT: Adams, Robyn L.
APPLICANT: Jespers, Stephen R.
TITLE OF INVENTION: TESTIS-SPECIFIC INSULIN HOMOLOG POLYPEPTIDES
NUMBER OF SEQUENCES. 1
APPLICANT: Lofton-Day, Catherine E. APPLICANT: Jaspers, Stephen R. TITLE OF INVENTION: TESTIS-SPECIFIC INSULIN HOMOLOG POLYPEPTIDES NUMBER OF SEQUENCES: 13 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

46.2%; Score 61; DB 2; Length 213;
Best Local Similarity 50.0%; Pred. No. 0.43;
Matches 10; Conservative 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING PC-TOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,267
```

ö

Gaps

ö

8; Indels

Mismatches

5 GLSSSCCKWGCSKSEISSLC 24

9; Conservative

```
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δλ
                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Adams, Robyn L.
APPLICANT: Jelmberg, Anna C.
APPLICANT: Lofton-Day, Catherine E.
APPLICANT: Jaspers, Stephen R.
TITLE OF INVENTION: TESTIS-SPECIFIC INSULIN HOMOLOG POLYPEPTIDES
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                     46.2%; Score 61; DB 4; Length 213; 50.0%; Pred. No. 0.43; tive 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                     NAME: SAWISIAK, DEDORAH A.
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 96-06
TELEPHONE: 206-442-6672
TELEPHONE: 206-442-6678
INPORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/905,267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A.
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 96-06
TELECOMMUNCATION INFORMATION:
TELEPHONE: 206-442-6672
TELEPAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08905267
Patent No. 5959075
GEBERAL INFORMATION:
APPLICANT: Lok, Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lok, Si
APPLICANT: Conklin, Darrell C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          173 GYSEKCCLTGCTKEELSIAC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                    5 GLSSSCCKWGCSKSEISSLC 24
                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                     LENGTH: 213 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 50.0%
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-09-314-051-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-905-267-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 536
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-905-267-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

DB 2; Length 188;

Score 59; DB 2 Pred. No. 0.7;

44.78;

Query Match Best Local Similarity

```
Gaps
                                                                                                                                                                 APPLICANT: LOK, SI
APPLICANT: Conklin, Darrell C.
APPLICANT: Adams, Robyn L.
APPLICANT: Jelmberg, Anna C.
APPLICANT: Jofton-Day, Catherine E.
APPLICANT: Joston-Day, Catherine E.
APPLICANT: Jespers, Stephen R.
TITLE OF INVENTION: TESTIS-SPECIFIC INSULIN HOMOLOG POLYPEPTIDES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

44.7%; Score 59; DB 4; Length 188;
Best Local Similarity 45.0%; Pred. No. 0.7;
Matches 9; Conservative 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: HENNER, DENNIS J.; VANDLEN, RICHARD L.; WILKINS, 171LE OF INVENTION: PROCESS AND COMPOSITIONS FOR THE NUMBER OF SEQUENCES: 42 CURRENT APPLICATION DATA: APPLICATION DATA: PRING DATE: 01-JUL-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/314,051
                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                          ; Sequence 2, Application US/09314051; Patent No. 6183991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A.
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 96-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
163 GFADKCCAIGCSKEELAVAC.182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 GFADKCCAIGCSKEELAVAC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 GLSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-09-314-051-2
                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  Abbar.
STREET: 120.
TTY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Patent No. 5464756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98102
                                                                                    US-09-314-051-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5464756-4
```

```
US-08-442-248-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: HENNER, DENNIS J.; VANDLEN, RICHARD L.; WILKINS,
JAMES A.; XANSURA, DANIEL G.
TITLE OF INVENTION: PROCESS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: PROCESS AND COMPOSITIONS FOR THE
LICHARD RELAXIN
NUMBER OF SEQUENCES: 42
CURRENT APPLICATION DATA:
PRIOR APPLICATION NUMBER: 347,550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 43.2%; Score 57; DB 6; Length 24; Local Similarity 47.4%; Pred. No. 0.18; Asservative 3; Mismatches 7; Indels
                                                                                                                                            43.9%; Score 58; DB 6; Length 22;
47.4%; Pred. No. 0.12;
tive 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: FastSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/950,720A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: CONKLIN, DARTELL C.
APPLICANT: Lofton-Day, Catherine E.
APPLICANT: Lok, Si
APPLICANT: Jaspers, Stephen R.
TITLE OF INVENTION: INSULIN HOMOLOG
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: ZymoGenetics, Inc.
1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08950720A
Patent No. 6046028
APPLICATION NUMBER: 347,550
FILING DATE: 04-MAY-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 LSGOCCHIGCTRRSIAKLC 24
                                                                                                                                                                                                                                          6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                   4 LSEKCCQVGCIRKDIARLC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                Ouery Match
Best Local Similarity 47.4%
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 120-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                    5464756-5; Patent No. 5464756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , LENGTH: 24
5464756-5
                                                              LENGTH: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-950-720A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                           SEQ ID NO:4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO:5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loca
Matches
                                                                                     5464756-4
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                          43.2%; Score 57; DB 3; Length 135;
47.4%; Pred. No. 0.93;
tive 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Caras, Ingrid W.
APPLICANT: Winslow, John W.
TITLE OF INVENTION: AL-1 Neurotrophic Factor NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA: US/08/442,248 FILING DATE: 15-MAY-1995 CLASSIFICATION 435 PRIOR APPLICATION DATA: APPLICATION DATA: PILING PAMEN: 08/330128 FILING PAMEN UMBER: 08/330128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 27-CCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: TOICHIA TIMOTHY E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 920C4
TELECOMMUNICATION INFORMATION:
TELEFRAN: 415,925-8674
TELEK: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08442248
Patent No. 5759863
               ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
                                                                          REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 LQTLCCTDGCSMTDLSALC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 928 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 47.49
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US.
ZIP: 94080
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                   US-08-950-720A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-442-248-2
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
```

```
δŏ
43.2%; Score 57; DB 1; Length 928; 57.9%; Pred. No. 5.8; tive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43.2%; Score 57; DB 1; Length 928; 57.9%; Pred. No. 5.8; tive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Caras, Ingrid W. APPLICANT: Winslow, John W. TITLE OF INVENTION: AL-1 Neurotrophic Factor NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS: ADDRESSE: Genentech, Inc. STREET: 460 Point San Bruno Blvd CITY: South San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Generach)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,815
FILING DATE: 15-MAY-1995
CLASSIFICATION ATA:
APPLICATION NUMBER: 08/330128
FILING DATE: 27-OCT-1994
ATFORNEY/AGENT INFORMATION:
NAME: TOTCHIA, TIMOTHY E.
REGISTRATION NUMBER: 36,700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08486449
Patent No. 6280732
Patent No. 6280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 2, Application US/08440815; Patent No. 5798448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                           485 LSGSCCECGCGRA--SSLC 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 415/225-8674
TELERAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                         6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      485 LSGSCCECGCGRA--SSLC 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    928 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                  11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 57.98
Matches 11; Conservative
                                    Best Local Similarity
Matches 11; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94080
                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-440-815-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-440-815-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
US-08-486-449-2
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                      RESULT
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43.2%; Score 57; DB 4; Length 928; 57.9%; Pred. No. 5.8; tive 3; Mismatches 3; Indels
                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
COMPATER: PROFING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
ZIP: 10591
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,537A
TLING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 103, Application US/08469537A
Patent No. 5843749
GENERAL INFORMATION:
APPLICANT: Maisonpierre, et al.
TITLE OF INVENTION: EHK AND ROR TYROSINE
TITLE OF THE OF TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: USSN 08/406,247
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: USSN 08/144,992
FILING DATE: 28-0CT-1993
APPLICATION NUMBER: USSN 07/736,559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/486,449
FILING DATE: 06-UNN-1995
CLASSIPECATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/330128
FILING DATE: 27-CCT-1994
ATTORNEY/AGENT INFORMATION:
: 460 Point San Bruno Blvd
South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P0920P1
TELEPHONICATION INFORMATION:
TELEPHONE: 415/225.9874
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415/952-981
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 928 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             485 LSGSCCECGCGRA--SSLC 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 57.99
Matches 11; Conservative
                                                                                     California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: ///
STRY: Tarrytown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                      USA
                                                                                                                                                                 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
US-08-469-537A-103
                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: N
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-486-449-2
```

9

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
5464756-1
; Patent No. 5464756
; Patent No. 5464756
; JAMES A.;YANSURA, DANNEL G.
; TITLE OF INVENTION: PROCESS AND COMPOSITIONS FOR THE
; ISOLATION HUMAN RELAXIN
; UNRBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/908,766
; FILING DATE: 01-101-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 347,550
; FILING DATE: 04-MAY-1989
; SEQ ID NO:1:
                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match

43.2%; Score 57; DB 2; Length 1005;
Best Local Similarity 57.9%; Pred. No. 6.3;
Matches 11; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match

42.4%; Score 56; DB 6; Length 24;
Best Local Similarity 42.1%; Pred. No. 0.24;
Matches 8; Conservative 4; Mismatches 7; Indels
FILING DATE: 26-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kempler, Ph.D., Gail M
REGISTRATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: REG 070C
TELECOMONICATION INFORMATION:
TELEPHONE: 914-345-7400
TELEFAX: 914-345-7721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: June 27, 2002, 16:08:44 Job time: 193 sec
                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 1005 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              596 LSGSCCECGCGRA--SSLC 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 LSNKCCHIGCTKKSLAKFC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: protein US-08-469-537A-103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5464756-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         οy
```

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

June 27, 2002, 16:09:27; Search time 36.01 Seconds (without alignments) 64.042 Million cell updates/sec Run on:

1 DVLAGLSSSCCKWGCSKSEISSLC 24 US-09-781-077-2_COPY_119_142 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:* PIR_71:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

٠.	Description		relayin - aniny do	Y DESC	1018		5	1		ם		relaxin precursor			H T		insulin homolog ce	relaxin precursor	brain-specific kin	hypothetical prote	•	relaxin - gorilla	-re	relaxin 2 precurso	relaxin 2 precurso	tic		֚֝֞֝֜֝֓֞֜֝֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֡֓֓֓֓֓֓֡֓֡֓֡֓֡֓֡֓			endo-1 4-bets	relavin - li++10.	
SUMMARIES	OI OI		A26463	A49739	RXRKOT	B58793	10000 K	A32201	102200	A53870	PYPH	C51602	20103	24/409	010010	837770	13/32/	A34936	14896/	507756	342/80	542/84	543224	542/86	A60982	\$00951	E83237	I47053	T21586	T34472	7	A29543	
	DB	: 1	~	~	Н	~		4 0	٦,	٠,	٠.	۱ ر	ا د	۹ ۲	۱ د	4 (۹ (۷ (7 (4 (۹ (v (7 (7	~	7	~	7	7	
	Length		54	48	44	22	l K	¥ 4	183	ď	186	200	808	1005	202	* 0	101	10	7 7 0	177	* [7 7 7	C # T	0 1	185	63	1159	143	399	823	448	64	
dФ	Query	1 (٠	•	•	•	~	 . m			٠,	~	· ~	· ~		3	, c V	٠.	10	7.05	١o	70	no	٠ د	n c	0.85	œ.	\sim	7	7	37.5	37.1	
	Score		* 1	99	63	58	28	28	58	57	57	57	57	57	56	256	71.0	n C	7 (200	5.5	1 1	4 5	, L	2 -	7 :	7.7	20	20	S	49.5	49	
	Result No.	-	٦ (7	m	4	2	9	7	89	6	10	11	12	13	14	15	19	17	18	19	20	22	22	3 6	7 6	# L	52	56	27	28	29	

ultra high-sulfur	relaxin precursor	fibrillin-1 propie	motellethin precur	merallorulouelu -	relaxin - quinea n	hypothetical pacts	hippoinetteat proce	nypornerical profe	Surface protein 51	ineniin 2 - toadfi	TIPECT 7 TOTAL	TUSATID - GACKBILL	metallothionein -	hombayin A-1 homel	tound at a monda	7 BOTOMON NTTRENT	thionin variant Th	Tombia describing I	ALL-IIL LISUI PIUS LIN	thionin variant Th
18946	S48082	5624	723		1194	1851	T42979	100	2002	102	2500	0 0	333	J00902	543582	1 0	55.2549	0.24		552545
S18	S48	A55	5	,	A4	TO	TA	· C	7	ENI	263	0 0	Š	g	5.43	1	35	A53		222
-	~	7	~	1	7	7	c	1	٧	Н	c	1	7	N	C	1 (7	~		7
169	182	2871	09	,	160	332	444	2222	777	20	5	1 (00	66	108	-	PΤΤ	131	100	130
۲.	37.1	۲.	4.		4.	4.	7			9.	9			9.	9	u	0	9.	ų	0.
37	3	37	36	20	30	36	36	36		32	35) (35	35	3	0	35	2	Ċ
9.	49	49	48	0 7	4	48	48	48	2 !	47	47	7.7	- I	47	47	7	ř	47	7.7	ř
30	7 :	32	33	2	* 1	32	36	37		æ	<u>چ</u>	9			2	ď	2 .	4	Ľ	2

ALIGNMENTS

A26463	
relaxin - spiny dogfish (frz C;Species: Squalus acanthias C;Date: 19-Nov-1988 #sequenc C;Accession: B26463; A26463	relaxin - spiny dogfish (fragments) C.Species: Squalus acanthias (spiny dogfish) C.Date: 19-Nov-1988 #sequence_revision 26-May-1995 #text_change 26-May-1995 C.Accession: B26463; A26463
R;Bullesbach, I Eur. J. Biochen	R;Bullesbach, E.E.; Gowan, L.K.; Schwabe, C.; Steinetz, B.G.; O'Byrne, E.; Callard, Eur. J. Biochem. 161, 335-341, 1986
A; Title: Isolation, A; Reference number: A; Accession: B26463	A.Title: Isolation, purification, and the sequence of relaxin from spiny dogfish (Squ A;Reference number: A91179; MUID:87054035 A;Accession: B26463
A; Molecule type: protein A; Residues: 'E', 2-30 <bul></bul>	: protein ,2-30 <bul></bul>
A; Experimental source: ovary A; Note: the amino-terminal ray Accession: A26463	A:Experimental source: ovary A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we h A:Accession: A26463
A; Molecule type: protein A; Residues: 31-54 <bu2></bu2>	: protein 54 <bu2></bu2>
C; Superfamily: insulin	source: ovary insulin
C; Keywords: hor F; 1-30, 31-54/Pr	C;Keywords: hormone; pyroglutamic acid F;1-30,31-54/Product: relaxin #status experimental <mat></mat>
F;1-30/Domain: F;31-54/Domain:	F:1-30/Domain: chain B #status experimental <chb></chb>
F;1/Modified si F;13-41,25-54,4	F:1/Modified site: pyrrollidone carboxylic acid (Gln) #status experimental F:13-41,25-54,40-45/Disulfide bonds: #status madiated
Query Match	56.1%;
Best Local Similarity Matches 11; Conserva	Best Local Similarity 55.0%; Pred. No. 0.0024; Consor 1; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
Qy 5 GLSSS	CCKWGCSKSEISSLC 24
Db 35 GMSSK	35 GMSSKCCTYGCTRKDISILC 54

relaxin - horse (fragments)

C:Species: Equus caballus (domestic horse)
C:Species: Equus caballus (domestic horse)
C:Date: 07-Apr-1994 #sequence_revision 26-May-1995
C:Accession: B49739; A49739
R:Stewart, D.R.; Nevins, B.; Hadas, E.; Vandlen, R.
Endocrinology 129, 375-383, 1991
A;Title: Affinity purification and sequence determination of equine relaxin. A;Reference number: A40739; MUID:91275796
A;Molecule type: protein
A;Residues: 1-28 <STE>
A;Accession: A49739
A;Molecule type: protein

ö

Gaps

; 0

Indels

9

```
47.4%; Pred. No. 0.18;
                          4; Mismatches
                                                                                                                                                                                                                                                                                    relaxin - Bryde's whale (fragments)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             relaxin - minke whale (fragments)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36 LSEKCCQVGCIRKDIARLC 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 LSEKCCQVGCIRKDIARLC 54
                                                                                                                                     4 LSEKCCQVGCIRKDIARLC 22
                                                                                   6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 47.4%
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 47.44
Matches 9; Conservative
                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: B32201
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1.54 <SCH>
C; Superfamily: insulin
Best Local Similarity
Matches 9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein A; Residues: 1-54 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-54 <SCH>C; Superfamily: insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: A32201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                              g
                                                                                            δ
           A;Residues: 29-48 <ST2>
C;Superfamily: insulin
C;Keywords: hormone; pyroglutamic acid
C;Keywords: hormone; pyroglutamic acid
C;Reywords: hormone; pyroglutamic acid
F;1-28,29-48/Product: relaxin #status experimental <CHB>
F;1-28,90main: chain B #status experimental <CHB>
F;29-48/Domain: chain A #status experimental <CHB>
F;29-48/Domain: chain A #status experimental <CHB>
F;1-28/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experim F;10-34,22-39,35-48/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R.Gowan, L.K.; Reinig, J.W.; Schwabe, C.; Bedarkar, S.; Blundell, T.L. FEBS Lett. 129, 80-82, 1981
A;Title: On the primary and tertiary structure of relaxin from the sand tiger shark (Odd A;Reference number: A01616; MUID:82004703
A;Reference number: A01616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Title: Isolation, purification, and the sequence of relaxin from spiny dogfish (Squalu A) Reference number: A91179; MUD:87054035
A) Contents: annotation; sequence revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 1;2-19;21-44 <GOW>
B; Bullesbach, E.E.; Gowan, L.K.; Schwabe, C.; Steinetz, B.G.; O'Byrne, E.; Callard, I.P.
Bur. J. Blochem, 161, 335-341, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Woods, A.S.; Cotter, R.J.; Yoshioka, M.; Buellesbach, E.; Schwabe, C. Int. J. Mass Spectrom. Ion Process. 111, 77-88, 1991
A;Title: Enzymatic digestion on the sample foil as a method for sequence determination A;Reference number: A58793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Note: the carboxyl-terminal sequence of chain B was determined to be Arg-Trp C; Superfamily: insulin C; Keywords: pyroglutamic acid C; Keywords: pyroglutamic acid C; Keywords: pyroglutamic acid B (fragments) #status experimental <CHB> F; 1-14/Domain: chain B (fragments) #status experimental <CHA> F; 1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental F; 3-31,15-44,30-35/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                relaxin chain A - Dall's porpoise
C;Species: Phocoenoides dalli (Dall's porpoise)
C;Date: 07-Aug-1998 #sequence_revision 07-Aug-1998 #text_change 21-Nov-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   relaxin - sand tiger (tentative sequence) (fragments)
C;Species: Odontaspis taurus (sand tiger)
C;Date: 01-Sep-1981 #sequence_revision 26-May-1995 #text_change 31-Mar-2000
C;Accession: A01616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                       50.0%; Score 66; DB 2; Length 48; 47.4%; Pred. No. 0.027; tive 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47.7%; Score 63; DB 1; Length 44;
52.6%; Pred. No. 0.064;
tive 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :| || :||:| :|| || 26 MSIKCCIYGCTKKDISVLC 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 LSHKCCYWGCTRKELAROC 48
                                                                                                                                                                                                                                                                                                                                                                                                                 6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 52.6
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                             Best Local Similarity 47.4 Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-22 <WOO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Superfamily: insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: B58793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: B58793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dp
                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
```

DB 2; Length 22;

43.9%; Score 58;

Query Match

```
relaxin precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 18-Jun-1999
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 18-Jun-1999
C;Accession: A90934; A93187; A90205; A90196; S32313; S32312; A29796; A01615
C;Accession: A90934; A90205; A90196; S32313; S32312; A29796; A01615
B;Haley J; Hudson, P; Scanlon, D; John, M; Cronk, M; Shine, J; Tregear, G; Ni
DNA 1, 155-162, 1982
A;Title: Porcine relaxin: molecular cloning and cDNA structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
C;Date: 31-Uul-1989 #sequence_revision 31-Jul-1989 #text_change 18-Jun-1993
C;Accession: B32201
R;Schwabe, C; Buellesbach, E.E.; Heyn, H.; Yoshioka, M.
B;Schwabe, C; Buellesbach, E.E.; Heyn, H.; Yoshioka, M.
A; Biol. Chem. 264, 940-943, 1989
A; Title: Cetacean relaxin. Isolation and sequence of relaxins from Balaenoptera acuto
A;Reference number: A32201; MUID:89093167
C; Species: Balaenoptera edeni (Bryde's whale)
C; Date: 31-Uul-1989 #sequence_revision 31-Jul-1989 #text_change 18-Jun-1993
C; Accession: A32201
R; Schwabe, C; Buellesbach, E.E.; Heyn, H.; Yoshioka, M.
B; Diol. Chem. 264, 940-943, 1989
A; Title: Cetacean relaxin. Isolation and sequence of relaxins from Balaenoptera acuto A; Reference number: A32201; MUID:89093167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.9%; Score 58; DB 2; Length 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.9%; Score 58; DB 2; Length 54; 47.4%; Pred. No. 0.36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 0.36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: A90934
A; Molecule type: DNA
A; Residues: 1-182 <HAL>
```

```
C; Species: Rattus norvegicus (Norway rat)
C;Date: 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 24-Sep-1999
C;Accession: A01614
R;Hudson, P.; Halley, J.; Cronk, M.; Shine, J.; Niall, H.
Nature 291, 127-131, 1981
A;Title: Molecular cloning and characterization of cDNA sequences coding for rat rela
A;Reference number: A01614; MUID:81197624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-186 <HUD>
A; Cross-references: GB:J00780; GB:M25468; NID:g206606; PIDN:AAA42029.1; PID:g206607
C; Superfamily: insulin
C; Superdamily: insulin
C; Superdamily: insulin
C; Superdamily: signal sequence #status predicted <SIG>
F; 1-22/Domain: signal sequence #status predicted <RNB>
F; 23-57/Domain: relaxin chain #status predicted <RNB>
F; 23-57/Domain: relaxin chain #status predicted <MAT>
F; 53-57/Bomain: relaxin chain A #status predicted <RNC>
F; 163-186/Domain: relaxin chain A #status predicted <RNA>
F; 163-186/Domain: plaxin chain A #status predicted <RNA>
F; 163-Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predi
                                                                                      C.Species: Can's lupus familiaris (dog)
C.Species: Can's lupus familiaris (dog)
C.Date: 27-Sep-1994 #sequence_revision 26-May-1995 #text_change 26-May-1995
C.Accession: B53879; A53879
R.Stewart, D.R.; Henzel, W.J.; Vandlen, R.
J. Protein Chem. 11, 247-253, 1992
A.Title: Purification and sequence determination of canine relaxin.
A.Accession: B53879
A.Molecule type: protein
A.Molecule type: prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.2%; Score 57; DB 2; Length 59; 42.1%; Pred. No. 0.53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 57; DB 1; Length 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | :| || ||::|:|| | 41 MSDKCCNVGCTRRELASRC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168 LSEQCCHIGCTRRSIAKLC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 47.40,
Best Local Similarity 47.40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                              - dog (fragments)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               relaxin precursor - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                 A; Molecule type: protein
A; Residues: 25-50, TwGR':161-182 <JAM>
R; Schwabe, C.; McDonald, J.K.; Steinhetz, B.G.
B; Schwabe, C.; McDonald, J.K.; Steinhetz, B.G.
B; Schwabe, C.; McDonald, J.K.
A; Reference number: A90205; MUD:77157271
A; Meference number: A90205; MUD:77157271
A; McCession: A90205
A; McCession: A90205
A; McCession: Appending the B-chain of porcine relaxin.
A; Residues: 25-47, VW, 50 <SCHI>
B; Schwabe, C.; McDonald, J.K.
B; Schwabe, C.; McDonald, J.K.
B; Schwabe, C.; McDonald, J.K.
A; Title: Demonstration of a pyroglutamyl residue at the N terminus of the B-chain of por A; Reference number: A90201; MUD:77134136
A; Contents: annotation pyrrolidone carboxylic acid
B; Schwabe, C.; McDonald, J.K.; Steinetz, B.G.
A; Title: Primary structure of the A chain of porcine relaxin.
A; Reference number: A90196; MUD:76231539
A;Cross-references: GB:K01088; NID:g164634; PIDN:AAA31114.1; PID:g164635
R;James, R.; Niall, H.; Kwok, S.; Bryant-Greenwood, G.
Mature 267, 544-546, 1977
A;Title: Primary structure of porcine relaxin: homology with insulin and related growth A;Reference number: A93187; MUID:77213067
A;Accession: A93187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A. Accession: A90196
A. Molecule type: protein
A. Residues: 161-169, E. 171-182 <SCH>
B. Schwabe, C.; McDonald, J.K.
A. Tritle: Relaxin: a disulfide homolog of insulin.
A. Reference number: A94245; MUID:77236040
A. Contents: annotation; disulfide bonds
A. Rontents: annotation; disulfide bonds
A. Contents: annotation; disulfide bonds
A. Contents: annotation; disulfide bonds
A. Tritle: Endogenous heterogeneity of relaxin and sequence of the major form in pregnant
A. Reference number: S32312; MUID:93257096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F.25-56/Domain: relaxin chain B **status experimental <RCB>
F.25-56/161-182/Poroduct: relaxin **status experimental <AMT>
F.161-182/Domain: relaxin chain A **status experimental <AMT>
F.25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) **status experimental F:34-169,46-182,168-173/Disulfide bonds: **status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-115,'L',117-182 <HA2>
A; Residues: 1-115,'L',117-182 <HA2>
C; Cross-references: GB: J02792; NID: 9164636; PIDN: AAA31115.1; PID: 9164637
C; Comment: Relaxin is an ovarian hormone that acts with estrogen to produce dilation of C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A Molecule type: protein
A/Residues: 161-182 (KO2)
Residues: 161-182 (KO2)
B. Haley, J.; Crawford, R.; Hudson, P.; Scanlon, D.; Tregear, G.; Shine, J.; Niall, J. Biol. Chem. 262, 11940-11946, 1987
A/Title: Porcine relaxin. Gene structure and expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43.9%; Score 58; DB 1; Length 182; 47.4%; Pred. No. 0.95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Superfamily: insulin
C; Keywords: pyroglutamic acid
F: 1.24/Domain: signal sequence #status predicted <SIG>
F: 25-56/Domain: relaxin chain B #status experimental <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             164 LSEKCCQVGCIRKDIARLC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein A; Residues: 25-53 <KOH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: S32313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S32312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: A29796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Introns: 70/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏ
```

ô

receptor-like tyrosine kinase Ehk-1 - rat

œ

1;

Gaps

7

```
A; Note: the authors translated the codon GAC for residue 170 as Glu
A; Note: the authors translated the codon GAC for residue 170 as Glu
C; Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea
C; Steywords: ATP; transmembrane protein
F; 675-941/Domain: protein kinase homology <KIN>
F; 683-691/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, September 1999
A; Description: MRNA for a putative insulin-like peptide of Caenorhabditis elegans.
A; Reference number: Z21691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          insulin homolog ceinsulin-3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Papio sp. (baboon)
C;Date: 06-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C;Accession: S42776
R;Evans, B.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:Z27106; NID:g415396; PIDN:CAA81622.1; PID:g415397
C;Genetics:
A; Note: the authors translated the codon GAC for residue 170 as Glu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Gene: rlx
S,Superfamily: insulin
C;Keywords: disulfide bond; hormone
F;1-24/Domain: relaxin chain A (fragment) #status predicted <RXA>
                                                                                                                                                                                                                                                                                                                                                                                      43.2%; Score 57; DB 2; Length 1005; 57.9%; Pred. No. 5; tive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.4%; Score 56; DB 2; Length 24; 42.1%; Pred. No. 0.36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, November 1995
A, Description: The sequence of C. elegans cosmid C17C3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: EMBL: AB032258; PIDN: BAA84470.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, November 1993
A;Reference number: S42776
A;Accession: S42776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
                                                                A;Status: preliminary
A;Molecule type: mrs, 359-1005 <MA2>
A;Residues: 1-305,'G', 359-1005 <MA2>
A;Cross-references: EMBL:S68026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         596 LSGSCCECGCGRA--SSLC 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 LSNKCCHIGCTKKSLAKFC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 42.1%
Local Similarity 42.1%
Local Similarity 42.1%
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 57.9%
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: T37327; T15535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          relaxin - baboon (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: Z18366
A; Accession: T15535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-91 <KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-24 < EVA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: T37327
                                           A; Accession: S51602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
         C; Species: Rattus norvegicus (Norway rat)
C; Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 28-May-1999
C; Accession: S51095 #sequence_revision 21-Jul-1995 #text_change 28-May-1999
C; Accession: Barrezueta, N.X.; Yancopoulos, G.D.
R; Maisonplerre, P.C.; Barrezueta, N.X.; Yancopoulos, G.D.
Oncogene 8, 3277-3288, 1993
A; Title: Ehk-1 and Ehk-2: two novel members of the Eph receptor-like tyrosine kinase fam A; Reference number: 849015; MUID:94067777
A; Accession: 851603
A; Accession: 851603
A; Residues: 1-893 < AMI>
A; Residues: 1-893 < AMI>
A; Residues: 1-893 < AMI>
A; Residues: Termanay
A; Noice: the authors translated the codon GAC for residue 170 as Glu
A; Note: the authors translated the codon GAC for residue 170 as Glu
C; Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat P
C; Superfamily: protein-tyrosine protein
F; 563-829/Domain: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Species: Rattus norvegicus (Norway rat)
C; Species: Rattus norvegicus (Norway rat)
C; Species: Rattus norvegicus (Norway rat)
C; Accession: 549015; 551602
R; Maisonpierre, P.C.; Barrezueta, N.X.; Yancopoulos, G.D.
R; Maisonpierre, P.C.; Barrezueta, N.X.; Yancopoulos, G.D.
A; Title: Eht. 1 and Eht. 2: two novel members of the Eph receptor-jike tyrosine Kinase fam A; Reference number: 549015; MUID:94067777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X78689; NID:9531543; PIDN:CAA55357.1; PID:9531544
A;Cross-references: EMBL:X78689; NID:9531544
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat C;Keywords: AFP; transmembrane protein protein protein kinase homology <KIN>
F;568-834/Demain: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 18-Jun-1999
C;Accession: S47489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43.2%; Score 57; DB 2; Length 898; 57.9%; Pred. No. 4.6; tive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43.2%; Score 57; DB 2; Length 893; 57.9%; Pred. No. 4.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 4.6;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor tyrosine kinase Ehk-1 - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            489 LSGSCCECGCGRA--SSLC 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          484 LSGSCCECGCGRA--SSLC 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:S68024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor tyrosine kinase - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Status: preliminary
A Molecule type: mRNA
A, Residues: 1-1005 <MAI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: S49015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S49015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
```

ö

Gaps

0;

```
relaxin precursor - rhesus macaque (;Species: Macaca mulatta (rhesus macaque) (;Species: Macaca mulatta (rhesus macaque) (;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #sequence_revision 07-Sep-1990 #sequence_revision 07-Sep-1990 #sequence_revision 07-Sep-1990 #sequence_revision 07-Sep-1990 #scrawford, R.J.; Hammond, V.E.; Roche, P.J.; Johnston, P.D.; Tregear, G.W. A.Title: Endocribol. 3, 169-174, 1989 A.Title: Structure of rhesus monkey relaxin predicted by analysis of the single-copy rhe A.Reference number: A34936; MUID:90073957
A; Residues: 1-91 <DUZ>
A; Residues: 1-91 <DUZ>
A; Cross-references: EMBL:U41279; NID:91086905; PID:91086914; PIDN:AAB52688.1; GSPDB:GN0G
A; Experimental source: strain Bristol N2; clone C17C3
C; Genetics:
A; Gene: C17C3.4
A; Map position: 2
A; Introns: 56/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                       .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 42.4%; Score 56; DB 2; Length 185; Best Local Similarity 42.1%; Pred. No. 1.8; Matches 8; Conservative 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                    Query Match
42.4%; Score 56; DB 2; Length 91;
Best Local Similarity 41.7%; Pred. No. 1;
Matches 10; Conservative 5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A Status: not compared with conceptual translation A; Molecule type: mRNA A; Rolecule type: mRNA C; Superfamily: insulin F;1-22/Domain: signal sequence #status predicted <SIG>F;23-185/Product: relaxin #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                | | | | : | | : | | : | | 56 DVLRRTASDCCRESCSLTEMLASC 79
                                                                                                                                                                                                                                                                                                                                                                                         1 DVLAGLSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167 LSNKCCHIGCTKKSLAKFC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                      QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
```

Search completed: June 27, 2002, 16:09:28 Job time: 212 sec

			•	
•				
				•
			•	
		·		
	•			
				•
				, K
·		•		

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on:

June 27, 2002, 16:16:52; Search time 18.68 Seconds (without alignments) 49.747 Million cell updates/sec

US-09-781-077-2_COPY_119_142 132 1 DVLAGLSSSCCKWGCSKSEISSLC 24 Title: Perfect score: Sequence:

105224 seqs, 38719550 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	P11953 squalus aca	969 equus ca	6			P58019 mus musculu		P11184 balaenonter			Q9y5q6 homo sapien	-	rattu	P54757 rattus norv	homo sa	_	_	Q60629 mus musculu	Q9qy05 mus musculu	P55848 procambarus					barle	dasya	P11952 raja erinac	_	371	171 mesoc	32	Q61554 mus musculu	136 sus
SOMETHES		OI .	RELX_SQUAC	RELX_HORSE	RELX_ODOTA	INL5_MOUSE	INL6_HUMAN	C59B_MOUSE	INL6_RAT	RELX_BALAC	RELX_BALED	RELX_PIG	INL5_HUMAN	RELX_CANFA	RELX_RAT	EPA5_RAT	EPA5_HUMAN	ILG1_CAEEL	RELX_MACMU	EPA5_MOUSE	INTOTAL	MIH_PROCL	YM17_PARTE	LIRP_LOCMI	RELZ_PANTR	KELZ_HUMAN	VINDIDA	KELX_DASSA	KELA_KAJER	INL3_CALJA	KRUA_HUMAN		RELX_MOUSE	- 1	FBN1_PIG
		Match Length DB		182 1													1037 1			101											י זע		185 1		
æ	Query	Match	9	0	47.7	7		45.1	•	٠	43.9	ς, γ	ή,	m (ή·	'n,	٠	· .	·ν·	41.7	0	> 0	2.04	ח כ	nα	n a	0 0	0 0	~ r	~ r	~ r	~ r	7.75		_
		score	74	99	69	63		59.5	53	28	28	100	0.1	7 .	70	0,	2/	0 1	0 1	0 4	r	0.0	U 1	7 0	20.0) L	4 1	10	7 5	n c	4 - V C		4.4	4. • V (4. V
	Result		н (N (η.	d i	٠ ک	ه ک	٠,	œ (ט נ	1.	7 C	77.	T T	+ 4	15	0 F	70	0 0	2 6	2 6	22	22	24.	25	90	2,0	ä	9 0	n (200	100	7 (ņ

RESULT 2 RELX_HORSE

P25127 P25127 P25128 P25127 P25128 P25127 P25128 P25127 P25128 P25128 P25128 P25128 P25128 P25128 P25722 P25722 P25722 P25722 P25723 P	DARD; PRT; 54 AA. 2, Created) 8, Last sequence update) 0, Last sequence update) 10, Last annotation update) 2, Created) 8, Last sequence update) 10, Last annotation update) 2, Created) 10, Last annotation update) 2, Last sequence update) 2, Chordata; Craniata; Vertebrata; Chondrichthyes; 10, Last annotation update) 2, Chordata; Craniata; Vertebrata; Chondrichthyes; 10, Last annotation vertebrata; Squalus. 11, 13, 13, 13, 14, 1986) 11, 11, 10, 10, 10, 10, 10, 10, 10, 10,	DB 1; 0.00028 ches
MT_ESOLU INL1_DROME RELX_CAVPO INS_BATSP INS_CORNAN MT2_CYPCA MTA_CYPS1 MTA_CYPS1 MT_CARAU MT_CARAU MT_CARAU MT_CARAU MT_CARAU	PRT; 54 ted) : sequence upda : annotation up togfish). ta; Craniata; qualoidei; Squaloidei; Squaloidei; Squaloidei; Squaloidei; Squaloidei; Squaloidei; Squaloidei; Squaloidei; Squaloidei; Squand the sequence. TRELAXIN INF. A B CHAIN AN Secreted. THE INSULIN/I 1. RELAXIN A C RELAXIN B C RELAXIN B C RELAXIN B C RELAXIN B C RELAXIN A C PYRROLIDONE INTERCHAIN. INTERCHAIN. INTERCHAIN. INTERCHAIN. INTERCHAIN.	Score 74; Pred. No.; Mismat.
ппппппппппппппппппппппппппппппппппппппп	Created) Last sequentiny dogfis tordata; Cea; Squalcea; TION OF A EER OF A	88; 5, 24 5, 5
134 134 160 50 60 60 60 60	STANDARD; PF 1. 12, Created) 1. 28, Last seque 1. 40, Last annot as (Spiny dogfish zoa; Chordata; Cr Squalea; Squaloi ; Gowan L.K., Sch Ification, and th s acanthias).; 161:335-341(198 HE FUNCTION OF RE LOCATION: Secret LOCATION: 1. HOWN: 1871 54 1 INTIT 54 1 I	56.1% Conservative KWGCSKSEISSLC : ::: TYGCTRKDISILC
88888888888888888888888888888888888888	ST (Rel. (Re	Similarity 1, Conser SSCCKWGCSK : : :: SKCCTYGCTR
44444444444444444444444444444444444444	1 QUAC CUAC 1-02-SQUAC 1-02-1989 1-FEB-1994 6-0-CT-2001 GOT-2001 GOT-2001 GOT-2001 GOT-2001 GOT-2001 GOT-2001 GOT-2001 GOT-2001 GOT-2001 GOT-2001 GOT-2001 GOT-2001 ISSUE-OVARY EDLINE-8705 UILESDE-NOT ISSUE-OVARY GOT-2001 ISSUE-OVARY ISSUE-OVARY GOT-2001 ISSUE-OVARY ISSUE-ING- I	atch cal Simi 11; GLSSSCC : GMSSKCC
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	RESULT STATE OF SERVICE STATE OF SERVICE STATE OF SERVICE SERV	Query M Best Lo Matches Qy 5

164 LSHKCCYWGCTRKELARQC 182

g

6 LSSSCCKWGCSKSEISSLC 24

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                     Klonisch T., Ryan P.L., Yamashiro S., Porter D.G.;
"Partial complementary deoxyribonucleic acid cloning of equine relaxin messenger ribonucleic acid, and its localization within the equine placenta.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stewart D.R., Nevins B., Hadas E., Vandlen R.;
"Affinity purification and sequence determination of equine relaxin.";
Endocrinology 129:375-383(1991).
-!- FUNCTION: RELAXIN IS AN OVARIAN HORMONE THAT ACTS WITH ESTROGEN
TO PRODUCE DILATATION OF THE BIRTH CANAL IN MANY MAMMALS.
-!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                         Būkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFIDE BONDS.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A -> V (IN REF. 2).
L -> Q (IN REF. 2).
E5C9414303A838B8 CRC64;
                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-HOKKAIDO; TISSUE-Placenta;
Min K., Shiota K., Ogawa T.;
"Molecular cloning of equine preprorelaxin cDNA.";
J. Reprod. Dev. 42:171-178(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONNECTING PEPTIDE. RELAXIN A CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RELAXIN B CHAIN.
           P22969; Q28907;
01-AUG-1991 (Rel. 19, Created)
01-ROV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
182 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A49739; A49739.

PIR; B49739; B49739.

HSSP; P01348; 4RLX.

InterPro; IPR000739; Insulin_IGF_relaxin.

SMART; SM00049; IIGF; 1.

PROSITE; PS00262; INSULN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91275796; PubMed=2055195;
                                                                                                                                                                                                                                                                                                                  MEDLINE=95359320; PubMed=7543295;
                                                                                                                                                                                                                                                                                                                                                                                         Biol. Reprod. 52:1307-1315(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insulin family; Hormone; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AB000201; BAA19069.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 26-53 AND 163-182.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; S78800; AAB35036.1; -.
                                                                                                                                                                                                                                                                                    SEQUENCE OF 32-174 FROM N.A.
                                                                          Prorelaxin precursor (RXN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20721
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156
182
169
182
173
66
                                                                                                          Equus caballus (Horse).
                                                                                                                                                       NCBL_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                           rissue-Placenta;
RELX HORSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
```

```
MEDILINE-62004703; PubMed=7274472; Gowan L.K., Reinig J.W., Schwabe C., Bedarkar S., Blundell T.L.; Gowan L.K., the primary and tertiary structure of relaxin from the sand tiger shark (Odontaspis taurus)."; FEBS Lett. 129:80-82(1981).
                                                                                                     Odontaspis taurus (Sand tiger shark) (Eugomphodus taurus).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Galeomorphii; Galeoidea; Lamniformes; Odontaspididae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                  "Isolation, purification, and the sequence of relaxin from spiny dogfish (Squalus acanthias) ";
Eur. J. Blochem. 161:335-341(1986).
-:- SUBDNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                      Bullesbach E.E., Gowan L.K., Schwabe C., Steinetz B.G., O'Byrne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09WUG6.
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Insulin-like peptide INSL5 precursor (Insulin-like peptide 5)
(Relaxin/insulin-like protein) (Relaxin/insulin-like factor 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
PIR; A01616; RXRKOT.
InterPor; IPRO00739; Insulin_IGF_relaxin.
Pfam: PF00049; Insulin; 1.
SMART; SM00078; I1GF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PYRROLIDONE CARBOXYLIC ACID. INTERCHAIN (BY SIMILARITY). INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.7%; Score 63; DB 1; Length 44; 52.6%; Pred. No. 0.0089; Live 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
6122F6604C660607 CRC64;
                                            11-JUL-1986 (Rel. 01, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RELAXIN A CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RELAXIN B CHAIN.
                PRT;
                                                                                                                                                                                                                                                                                                                            MEDLINE=87054035; PubMed=3780747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00078; ILGF; 1.
PROSITE; PS00262; INSULIN; 1.
Insulin family; Hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35
4730 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                              Relaxin (Fragments)
                                                                                                                                                         Carcharias.
NCBI_TaxID=30501;
                                                                                                                                                                                                                                                                                                            REVISION TO 20
                                                                                                                                                                                                                                                                                                                                                           Callard I.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INL5_MOUSE
                RELX_ODOTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
NON_CONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_CONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
INL5_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
RELX_ODOTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC
DT
DT
DE
                                ò
```

ö

;

Gaps

.; o

Query Match 50.0%; Score 66; DB 1; Length 182; Best Local Similarity 47.4%; Pred. No. 0.011; Matches 9; Conservative 4; Mismatches 6; Indels

```
RESULT 5
INL6_HUMAN
                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                    Submitted (UUL-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MAY HAVE A ROLE IN GUT CONTRACTILITY OR IN THYMIC
DEVELOPMENT AND REGULATION.
-!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
DISULFIDE BONDS (BY SIMILARITY).
-!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN COLON WITH LOWER LEVELS
IN THYMUS. MIMIMAL LEVELS IN TESTIS.
-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                    MEDLINE-99389725; PubMed-10458910; Conklin D., Lofton-Day C.E., Haldeman B.A., Ching A., Whitmore T.E., Lok S., Jaspers S.; Jaspers S.; "Identification of INSL5, a new member of the insulin superfamily."; Genomics 60:50-56(1999).
                                                                                                                                                                                   Hsu S.Y.; "Cloning of two novel mammalian paralogs of relaxin/insulin family proteins and their expression in testis and kidney."; Mol. Endocrinol. 13:2163-2174(1999).
                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
INSULIN-LIKE PROTEIN INSL5 B CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INSULIN-LIKE PEPTIDE INSUS A CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
CONNECTING PEPTIDE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05FF9A0F613DBF92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF076971; AAD48089.1; --
EMBL; AF054842; AAF08093.1; ALT_INIT.
EMBL; BC010968; AAF08094.1; --
EMBL; BC010968; AAH10968.1; --
MGD; MGI:1346085; Ins15.
INTERPO; IPF000799; Insulin_IGF_relaxin.
SMARY; SM00078; IlGF; 1.
                                                                SEQUENCE FROM N.A., AND TISSUE SPECIFICITY
                                                                                                                                                              STRAIN=FVB; TISSUE=Ovary;
MEDLINE=20065648; Pubmed=10598589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insulin family; Hormone; Signal.
 INSL5 OR ZINS3 OR RIF2 OR RIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF133817; AAD29687.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 II
135 II
126 B)
15524 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114
             Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135 AA;
                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49
115
                                                                                                                                                                                                                                                              Strausberg R.;
                                                                            TISSUE=Colon;
                                                                                                                                                                                                                                                    TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
```

MEDLINE—20297000; Pubmed=10819760; Defton-Day C.E., Adams R.L., Jolmston D.S., Conklin D., Lofton-Day C.E., Griswold M.D., Josepers S.R.; and Instituted in the testis of the human and Rat."; Expressed in the testis of the human and Rat."; BLONTION: April 2593-1599 (2000).

1. FUNCTION: MAY HAVE A ROLE IN SPERM DEVELOPMENT AND FERTILIZATION.

1. SUBCELLUIAR LOCATION: Secreted (By similarity).

1. TISSUE SPECIFICITY: TESTIS-SPECIFIC.

1. SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.

"Cloning of two novel mammalian paralogs of relaxin/insulin family proteins and their expression in testis and kidney."; Mol. Endocrinol. 13:2163-2174(1999).

SEQUENCE FROM N.A.

TISSUE-Testis;

MEDLINE=20065648; PubMed=10598589;

SEQUENCE FROM N.A.

TISSUE=Testis;

NCBI_TaxID=9606;

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Homo sapiens (Human).

INSL6 OR RIF1.

UNIC HUMAN STANDARD; PRT; 213 AA.
09Y581; 09NS16;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2002 (Rel. 41, Last annotation update)
10-MAR-2002 (Rel. 41, Last annotation update)
Insulin-like peptide INSL6 precursor (Insulin-like peptide

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                               Insulin family; Hormone; Signal; Cleavage on pair of basic residues.
                                                                                                                                                                                                                                                                                                                                                                                      INSULIN-LIKE PEPTIDE INSL6.
INSULIN-LIKE PROTEIN INSL6 B CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
INSULIN-LIKE PROTEIN INSL6 A CHAIN
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
INSULIN-LIKE PROTEIN INSL6 C CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.2%; Score 61; DB 1; Length 213; 50.0%; Pred. No. 0.066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -> K (IN REF. 1).
8BA0976F660ACE8B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 0.06
2; Mismatches
                                                                                                                                                                                                                                              InterPro; IPR000739; Insulin_IGF_relaxin.
Bam, PR00049; Insulin, 1.
SMART; SMO0078; IIGF; 1.
PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ъ -
- к
                                                                                                                                                                               EMBL; AF135824; AAF29604.1; -. EMBL; AF156094; AAD39003.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24878 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 50.0°
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        53
                                                                                                                                                                                                                                                                                                                                                                                                                                                     168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146
213 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   55
                                                                                                                                                                                                                              MIM; 606414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROPEP
                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROPEP
                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
```

ö

Gaps

;

8; Indels

; 0

Gaps

.0

5; Indels

Score 63; DB 1; Length 135; Pred. No. 0.023; 4; Mismatches 5; Indels

47.78;

Query Match

Matches

52.6%;

117 LOALCCREGCSMKELSTLC 135

qq

6 LSSSCCKWGCSKSEISSLC 24 Local Similarity 52.6 sees 10; Conservative

```
Insulin-like peptide INSL6 precursor (Insulin-like peptide 6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Balaenopteridae; Balaenoptera.
NCBI_TaxID=9767;
                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF159506; AAD40956.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 GFADKCCAIGCSKEELAVAC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 GLSSSCCKWGCSKSEISSLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168
188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                         SEQUENCE FROM N.A.
                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RELX_BALAC
P11184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Relaxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RELX_BALAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
     Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OC OC OC OC OC
                                                                                                                                                                                                                                                                                        The Qian Y.-M., Oin X., Miwer T., Sun X., Halperin J.A., Song W.-C.;

RT Tidentification and functional characterization of a new gene encoding

RT The mouse terminal complement inhibitor CD59.";

LJ. Immunol. 165:2528-2534(2000).

CC OMPLEX (MAC) ACTION. ACTS BY BINDING TO THE CRAND/OR C9

COMPLEX (MAC) ACTION. ACTS BY BINDING TO THE CAND/OR C9

COMPLEX (MAC) ACTION. ACTS BY BINDING TO THE CAND/OR C9

COMPLEX (MAC) ACTION. ACTS BY BINDING TO THE CAND/OR C9

COMPLEX (MAC) ACTION. ACTS BY BINDING TO THE CAND/OR C9

COMPLEX (MAC) ACTION. ACTS BY BINDING TO THE CAND/OR C9

COMPLEX (MAC) ACTION. ACTS BY BINDING TO THE CAND/OR C9

COMPLEX (MAC) ACTION. ACTS BY BINDING TO THE CAND/OR C9

COMPLEX (MAC) ACTION. ACTS BY BINDING TO THE CAND/OR C9

COMPLEX (MAC) ACTION. ACTS BY BINDING TO THE CAND/OR COMPLETE

FORMATION OF THE OSMOLYTIC PORE (BY SIMILARITY).

C -- SUBCLIDIAR (CATION: Attached to the membrane by a GPI-anchor.)

C -- SIMPLEARIY: CONTAINS 1 UPAR/LY6 DOMAIN.

MCD: MGI:1888996; Cd59b.

R MCD: MGI:1888996; Cd59b.

R MCD: MGI:1888996; Cd59b.

R Ffam; PF0001; UPAR_LX6; 1.

R PCODOM; PD00128; LY6-CD59; 1.

R PCAMAT: SMON134: LY-6-CD59; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GPI-anchor; Signal.
POTENTIAL.
CD59B GLXCOPROTEIN.
REMOVED IN MATURE FORM (BY SIMILARITY).
                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                 16-007-2001 (Rel. 40, Created)
16-007-2001 (Rel. 40, Last sequence update)
16-007-2001 (Rel. 40, Last amontation update)
16-007-2001 (Rel. 40, Last amontation update)
CD59B glycoprotein precursor (Membrane attack complex inhibition factor) (MACIF) (MAC-inhibitory protein) (MAC-IP) (Protectin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 59.5; DB 1; Length 129; Pred. No. 0.071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UPAR/LY6.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTEN'
GPI-ANCHOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 188 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 LAGLSSSCCKWG-CSK-----SEISSL 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00134; LU; 1.
PROSITE; PS00983; LY6_UPAR; FALSE_NEG.
Antigen; Glycoprotein; GPI-anchor; Sig
                                                                                                                                                                                                                                                                                 MEDLINE=20405635; PubMed=10946279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14266 MW;
                      173 GYSEKCCLTGCTKEELSIAC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45.1%;
         5 GLSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107
107
107
36
62
62
86
92
39
                                                                                                                                                                                              Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                              C59B_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INL6_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9WV41;
                                                                                                          P58019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                       RESULT 6
C59B_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INL6_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DA LA LA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
                                                                                                           δ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                             Gaps
Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROMITE: PS00262; INSULIN: 1.
Insulin family; Hormone; Signal; Cleavage on pair of basic residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INSULIN-LIKE PEPTIDE INSL6.
INSULIN-LIKE PROTEIN INSL6 B CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
INSULIN-LIKE PROTEIN INSL6 C CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INSULIN-LIKE PROTEIN INSL6 A CHAIN
                                                                                                                                                               TISSUE-Testis; MEDLINE-20297000; PubMed-10819760; Lofton-Day C.E., Adams R.L., Lok S., Johnston D.S., Conklin D., Lofton-Day C.E., Adams R.L., Jelmberg A.C., Whitmore T.E., Schrader S., Griswold M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PYRROLIDONE CARBOXYLIC ACID (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44.7%; Score 59; DB 1; Length 188; 45.0%; Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50212AB3CE9982B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-1989 (Rel. 11, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR000739; Insulin_IGF_relaxin.
Pfam; PF00049; Insulin; 1.
SMART; SM00078; IIGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1989 (Rel. 11, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21442 MW;
```

ö

```
CHAIN
                                                                                                                                                                                                                                                                                                                                    10
                                                                                                                                                                                                                                                                                                                                                     RELX_PIG
                                                                                                                                                                                                                                                                                                                                    RESULT
                FFFFS
                                                                                                                                                                                                                                    Óλ
                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                 MEDLINE-89093167; PubMed-2910872; Schwabe C., Bullesbach E.E., Heyn H., Yoshioka M.; Schwabe C., Bullesbach E.E., Heyn H., Yoshioka M.; Chedean relaxin: Isolation and sequence of relaxins from Balaenoptera acutorostrata and Balaenoptera edeni."; J. Biol. Chem. 264:940-943(1989).
-!- FUNCTION: RELAXIN IS AN OVARIAN HORMONE THAT ACTS WITH ESTROGEN TO PRODUCE DILATATION OF THE BIRTH CANAL IN MANY MAMMALS.
-!- SUBBUNT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-89093167; PubMed-2910872; Schwabe C., Bullesbach E.E., Heyn H., Yoshioka M.; Schwabe C., Bullesbach E.E., Heyn H., Yoshioka M.; Cetacean relaxin. Isolation and sequence of relaxins from Balaenoptera acutorostrata and Balaenoptera edeni."; J. Biol. Chem. 264:940-943(1989).
-!- FUNCTION: RELAXIN IS AN OVARIAN HORMONE THAT ACTS WITH ESTROGEN TO PRODUCE DILATATION OF THE BIRTH CANAL IN MANY MANMALS.
-!- SUBBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                               -1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
PIR; B32201; B32201.
HSSP; P01348; 4RLX.
InterPro; IPR000739; Insulin_IGF_relaxin.
SMART: SM00078; Insulin; 1.
PROSITE; PS00262; INSULIN; 1.
Insulin family; Hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
PIR; A32201; A32201.
HSSP; P01348; 4RLX.
InterPro; IPR000739; Insulin_IGF_relaxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DC2672CB940F58BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 58; DB 1;
Pred. No. 0.055;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       RELAXIN B CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-001.1989 (Rel. 11, Created)
01-00L-1989 (Rel. 11, Last Sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                             RELAXIN A CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RELAXIN B CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERCHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Balaenoptera edeni (Bryde's whale).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Balaenopteridae; Balaenoptera.
                                                                                                                                                                                                                                                                                                                                                                                                                      33
54
41
54
45
6099 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00262; INSULIN; 1.
Insulin family; Hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36 LSEKCCQVGCIRKDIARLC 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 47.4%,
Local Similarity 47.4%,
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00049; Insulin; 1.
SMART; SM00078; ILGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RELX_BALED
[1]
SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                    NON_CONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Relaxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_CONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RELX_BALED
                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HD DT HD HD DT HD HD DT 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

```
ö
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schwabe C., McDonald J.K.; "Demonstration of a pyroglutamyl residue at the N terminus of the B-chain of porcine relaxin."; Blochem. Biophys. Res. Commun. 74:1501-1504(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDILINE-87308187; PubMed-2442155;
Haley J., Crawford R., Hudson P., Scanlon D., Tregear G., Shine J.,
Niall H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY SEQUENCE OF 25-54 AND 161-182.
MEDLINE-77213067; PubMed-876374;
James R., Niall H., Kwok S., Bryant-Greenwood G.;
"Primary structure of porcine relaxin: homology with insulin and
                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-83157118; PubMed-6897721;
Haley J., Hudson P., Scanlon D., John M., Cronk M., Shine J.,
Tregear G., Niall H.;
"Porcine relaxin: molecular cloning and cDNA structure.";
DNA 1:155-162(1982).
                                                                                                                                                                      Length 54;
                                                                                                                                                                                                                     6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 25-51.
MEDLINE=77157271; PubMed=851452;
Schwabe C., McDonald J.K., Steinetz B.G.;
"Primary structure of the B-chain of porcine relaxin.";
Biochem. Biophys. Res. Commun. 75:503-510(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=76231539; PubMed=938497;
Schwabe C., McDonald J.K., Steinetz B.G.;
"Primary structure of the A chain of porcine relaxin.";
Biochem. Biophys. Res. Commun. 70:397-405(1976).
                                                                                              DB5535F8951F49BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Porcine relaxin. Gene structure and expression.";
J. Biol. Chem. 262:11940-11946(1987).
                                                                                                                                                                 Score 58; DB 1;
Pred. No. 0.055;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
       RELAXIN A CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                 182 AA.
                                                 INTERCHAIN.
                             INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 25.
MEDLINE=77134136; PubMed=843375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=77236040; PubMed=887933; Schwabe C., McDonald J.K.;
54
41
54
45
6072 MW;
                                                                                                                                                                                     47.48;
                                                                                                                                                                    43.9%;
                                                                                                                                                                                                                                                           6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                       36 LSEKCCOVGCIRKDIARLC 54
                                                                                                                                                                                  Best Local Similarity 47.4 Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          related growth factors.";
Nature 267:544-546(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prorelaxin precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 161-182.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFIDE BONDS
                      DISULFID
DISULFID
                                                                   DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                          RELX_PIG
P01348;
                                                                                                                                                                    Query Match
```

```
MIM; 606413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RELX_CANFA
                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                           PROPEP
                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RELX_CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                   Nature 271:278-281(1978).
-!- FUNCTION: RELEAXIN IS AN OVARIAN HORMONE THAT ACTS WITH ESTROGEN TO PRODUCE DILATATION OF THE BIRTH CANAL IN MANY MAMMALS.
-!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                        MEDLINE-78092399; PubMed-622170; Isaacs N.W., James R., Niall H., Bryant-Greenwood G., Dodson G.G., Evans A., North A.C.T.; "Relaxin and its structural relationship to insulin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MX-2000 (Rel. 39, Created)
30-MX-2000 (Rel. 39, Last sequence update)
10-MXR-2002 (Rel. 41, Last annotation update)
101-MXR-2012 (Rel. 11, Last annotation update)
                                                                                                                                                I - SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43.9%; Score 58; DB 1; Length 182; 47.4%; Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                            CONNECTING PEPTIDE.
RELAXIN A CHAIN.
PYRROLIDONE CARBOXYLIC ACID.
INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G -> GVWS (IN REF. 4).
WGRT -> TWGR (IN REF. 3).
S -> L (IN REF. 1).
Q -> E (IN REF. 6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20736EB089F13AB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 Insulin family; Hormone; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                      RELAXIN B CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
  "Relaxin: a disulfide homolog of insulin.";
                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR000739; Insulin_IGF_relaxin.
Pfam; PF00049; Insulin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERCHAIN.
                                                                                                                                      SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                   EMBL; K01088; AAA31114.1; -... EMBL; J02792; AAA31115.1; -... EMBL; A16593; CAA01295.1; -... EMBL; A06652; CAA00600.1; -... PIR; A01615; RXPG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20818 MW;
                                                                                                                                                                                                                                                                                                                                                                                         PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 LSSSCCKWGCSKSEISSLC 24
              Science 197:914-915(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                              24
56
1154
1182
169
1182
                                                                                                                                                                                                                                                                                                                   PDB; 1RLX; 15-OCT-94.
PDB; 2RLX; 15-OCT-94.
PDB; 3RLX; 15-OCT-94.
PDB; 4RLX; 15-OCT-94.
                                   3D-STRUCTURE MODELING.
                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00078; ILGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           170
182 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                             DISULFIDE BONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INL5_HUMAN
Q9Y5Q6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                 PROPEP
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INSL5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
INL5_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ID DT DT OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in o way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                        DISULFIDE BONDS (BY SIMILARITY).
--- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN RECTUM WITH LOWER LEVELS
IN UTERUS AND ASCENDING AND DESCENDING COLON.
--- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                              CONKIN D., Lofton-Day C.E., Haldeman B.A., Ching A., Whitmore T.E., Lok S., Jaspers S.; "Identification of INSL5, a new member of the insulin superfamily."; Genomics 60:50-56(1999).
                                                                                                                                                                                                                                                                                                                                                     DEVELOPMENT AND REGULATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoà; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INSULIN-LIKE PEPTIDE INSL5 B CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INSULIN-LIKE PEPTIDE INSL5 A CHAIN
                                                                                                                                                                                                                                                                                                                   -! - FUNCTION: MAY HAVE A ROLE IN GUT CONTRACTILITY OR IN THYMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Placenta;
MEDLINE-99150177; PubMed-10026098;
Klonisch T., Hombach-Klonisch S., Froehlich C., Kauffold J.,
Steger K., Steinetz B.G., Fischer B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
CONNECTING PEPTIDE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.2%; Score 57; DB 1; Length 135; 47.4%; Pred. No. 0.17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERCHAIN (BY SIMILARITY). INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
98FFCB20E9C4BC1F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09TRM6 09TRM9; 09N027;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Mismatches
                                                                                                                  SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interproj 197000739; Insulin_IGF_relaxin.
SMART; SMO0078; IIGF; 1.
PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                            MEDLINE=99389725; PubMed=10458910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insulin family; Hormone; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF133816; AAD29686.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15318 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | : || ||| ::|||
117 LQTLCCTDGCSMTDLSALC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prorelaxin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 1
121 1
135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9615;
                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49
115
```

0;

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content; is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
 "Canine preprorelaxin: nucleic acid sequence and localization within the canine placenta.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murínae; Rattus.
                                                                                                                                               -!- FUNCTION: Relaxin is an ovarian hormone that acts with estrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-81197624; PubMed-7231533;
Hudson P., Haley J., Cronk M., Shine J., Niall H.;
"Molecular cloning and characterization of cDNA sequences coding for
                                                                                                                                                             to produce dilatation of the birth canal in many mammals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONNECTING PEPTIDE (BY SIMILARITY).
RELAXIN A CHAIN.
                                                                                                                                                                                               DISDURING DOWN.
-!- SUBCELULIAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Placenta; syncytiotrophoblast.
-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                    Stewart D.R., Henzel W.J., Vandlen R.; "Purification and sequence determination of canine relaxin."; J. Protein Chem. 11:247-253(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43.2%; Score 57; DB 1; Length 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     I -> S (IN REF. 2).
220BB0EC99DD302A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RELAXIN B CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000739; Insulin_IGF_relaxin.
Pfam; PF00049; Insulin; 1.
SMART; SM00078; IIGF; 1.
PROSITE: PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                       MEDLINE=93000391; PubMed=1388669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         insulin family; Hormone; Signal.
                        Biol. Reprod. 60:551-557(1999).
                                                          SEQUENCE OF 26-60 AND 154-177.
                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF233687; AAF60302.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20563 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        159 MSDKCCNVGCTRRELASRC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rat relaxin.";
Nature 291:127-131(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                    placenta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prorelaxin precursor.
                                                                                                                                                                                            DISULFIDE BONDS
                                                                                                                                                                                                                                                                                                                                                                                                    P01348; 4RLX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                          TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63
154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RELX_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P01347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    οy
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maisonpierre P.C., Barrezueta N.X., Yancopoulos G.D., "Ehk-1 and Ehk-2: two novel members of the Eph receptor-like tyrosine kinase family with distinctive structures and neuronal expression."; Oncogene 8:3277-3288(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                          implications for physiological studies.";
Endocrinology 108:726-729(1981).
-!- FUNCTION: RELARIN IS AN OVARIAN HORMONE THAT ACTS WITH ESTROGEN
TO PRODUCE DILATATION OF THE BIRTH CANAL IN MANY MAMMALS.
-!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Ephrin type-A receptor 5 precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor EHK-1) (EPH homology kinase-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 0
                                              John M.J., Borjesson B.W., Walsh J.R., Niall H.D.; "Limited sequence homology between porcine and rat relaxins:
                                                                                                                                                                     -:- SUBCELLULAR LOCATION: Secreted.
-:- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43.2%; Score 57; DB 1; Length 186;
47.4%; Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PYRROLIDONE CARBOXYLIC ACID.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / SIMILARITY,
08BAEC79BCF0E80F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONNECTING PEPTIDE. RELAXIN A CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4 AND 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RELAXIN B CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1005 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000739; Insulin_IGF_relaxin. Pfam; PF00049; Insulin; 1. SMART; SM00078; IIGF; 1. PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-SPRAGUE-DAWLEY; TISSUE-Brain;
MEDLINE-94067777; Pubmed-7504232;
                SEQUENCE OF 23-57 AND 163-188.
MEDLINE=81090283; Pubmed=7004862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Insulin family; Hormone; Signal.
                                                                                                                                                                                                                                                                                                                                                EMBL; J00780; AAA42029.1; -. EMBL; V01264; CAA24578.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20489 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168 LSEQCCHIGCTRRSIAKLC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57
158
186
163
173
177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPHAS OR EKHI OR EHK-1
                                                                                                                                                          DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
9; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186 AA;
                                                                                                                                                                                                                                                                                                                                                                                 PIR; A01614; RXRT.
HSSP; P01348; 4RLX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23
58
163
163
36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOD_RES
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EPA5_RAT P54757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROPEP
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EPA5_RAT
QQ
```

```
between the Swiss Institute of Bioinformatics and the EMBL outstation—
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR0010561; EGF-11ke.

InterPro; IPR0010561; EGF-11ke.

InterPro; IPR0010961; EML_pKinase.

InterPro; IPR003961; FN_III.

InterPro; IPR0013962; FN_III.

InterPro; IPR001426; FN_EDII_Lepeat.

InterPro; IPR001426; FN_EDII_Lepeat.

InterPro; IPR00144; EPH_1D64; I.

InterPro; IPR00145; IPR_III.

INTERPRO; IPR00145; IPR_III.

INTERPRO; IPR00146; IPR III.

INTERPRO; IPR00146; IPR III.

INTERPRO; IPR00146; IPR III.

INTERPRO; IPR00146; IPR III.

INTERPRO; IPR00146; IPR0FIII.

INTERPRO; IPR00146; IPR0044; II.

INTERPRO; IPR00146; IPR0644; II.

INTERPRO; IPR0644; IPR0644; II.

INTERPRO; IPR0644; IPR0644; IPR0644; II.

INTERPRO; IPR0644; IPR064
                                                                                                                                                                                                                                                                                               tyrosine phosphate.

-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- ALTERNATIVE PRODUCTS: 6 ISONEMS; 1 (SHOWN HERE), 2, 3, 4, 5 AND 6; ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: ALMOST EXCLUSIVELY EXPRESSED IN THE NERVOUS SYSTEM. PREDOMINANTLY EXPRESSED IN NEURONS.
-!- SIMILARITY: CONTAINS 1 SAM DOMAIN.
-!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
-!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
                                                                                                                     Lassmann H., Steck A.J.;
Lassmann H., Steck A.J.;
Lassmann H., Steck A.J.;
Lastression and developmental regulation of Ehk-1, a neuronal
Elk-like receptor tyrosine kinase in brain.";
Neuroscience 63:163-178(1994).
-!- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
EPHRIN-A1, -A2, -A3, -A4 AND -A5.
-!- CATALITIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                     WEDLINE-95206467; PubMed-7898646;
Taylor V., Miescher G.C., Pfarr S., Honegger P., Breitschopf H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
CYS-RICH.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BY SIMILARITY). (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                          STRAIN-SPRAGUE-DAWLEY; TISSUE-Brain;
[2]
SEQUENCE FROM N.A. (ISOFORM 6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000561; EGF-like.
InterPro; IPR001090; Ephrin_rec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X78689; CAA55357.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alternative splicing.
26GAL 1 26
CHAIN 27 575
DOMAIN 27 575
DOMAIN 597 1005
DOMAIN 597 1005
DOMAIN 222 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RECEPTOR SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
NP_BIND
RINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
```

```
ï
                                                                                                                                                                   VCRPGFFKASPHSQTCSKCPPHSYTHEEASTSCVCEKDYFR
                                                                                                                                                                                                                     KCNSHAGYCEEGGGHYRYLPQQIGLKNTSVMMADPLAHTNY
TFEIEAVNGVSDLSPGTRQYVSVNVTTNQAA -> T (IN
ISOFORM 3, ISOFORM 4, ISOFORM 5 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "cDNA cloning and tissue distribution of five human EPH-like receptor protein-tyrosine kinases.";
                                                                                                                                                                                                          RPPSAPRNAISNVNETSVFLEWIPPADTGGGKDVSYYILCK
       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (AUTO-) (POTENTIAL).
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COCCOGEN 10:897-905(1995).

-!- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO EPHRIN-A1, -A2, -A3, -A4 AND -A5.

-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Ephrin type-A receptor 5 precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor EHK-1) (Eph homology kinase-1) (Receptor protein-tyrosine kinase HEK7).
EPHAS OR EHK1 OR HEK7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                        N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                            GRRRTQGRGGG -> DADGPRAQASWCHARR (IN
                                                                                                                                                                                                                                                                            SGSCCECGCGRASSLCAVAHPSLIW -> R (IN
                                                                                                                                                                                   RESDPPTMACT -> G (IN ISOFORM 2 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Brain;
MEDLINE=55206782; PubMed=7898931;
FOX G.M., Holst P.L., Chute H.T., Lindberg R.A., Janssen A.M.,
Basu R., Welcher A.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;;
                                                                                                                                                                                                                                                                                                                                                                                                                       43.2%; Score 57; DB 1; Length 1005; 57.9%; Pred. No. 0.94;
                                                                                                                                                                                                                                                                                                   D -> E (IN REF. 2).
G -> A (IN REF. 2).
G -> A (IN REF. 2).
G -> A (IN REF. 2).
T -> I (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                         ISOFORM 4 AND ISOFORM 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1037 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                            ISOFORM 6)
                                                                                                                                                                                                                                                               ISOFORM 6)
                                                                                                                                                                                                   ISOFORM 5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 25-1037 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       596 LSGSCCECGCGRA--SSLC 612
                                                                                                                                                                                                                                                                                                                                                                                     111007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 57.93
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                       170
5566
578
669
708
979
802
6552
8352
8353
301
4423
463
20
                                                                                                                                                                                                                                                                                                        170 17
566 56
578 57
669 66
708 70
979 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                              358
                                                                                                                                                                                                                                                                                597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Miescher G.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPAS_HUMAN
                                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                VARSPLIC
                                                                                                                                                                                                                                                                                VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                          CARBOHYD
                                                                                                                                 CARBOHYD
                                                                                                                                                                        VARSPLIC
                                                                                                                                                                                                                                                                                                                                               CONFLICT
                                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
            MOD_RES
MOD_RES
MOD_RES
MOD_RES
                                                                CARBOHYD
                                                                                CARBOHYD
                                                                                           CARBOHYD
                                                                                                                      CARBOHYD
                                                                                                                                                VARSPLIC
                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPA5_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R PRINTS; PROD014; FUTUPELLI.

R PRINTS; PROD019; TYRTPELLI.

R PRINTS; PROD0109; TYRTPELLI.

R PRODON; PROD019; TYRTNASE.

R SWART; SW00001; EGF_11ke; 1.

R SWART; SW00001; EGF_11ke; 1.

R SWART; SW0019; PROFEIN.

R SWART; SW00119; TYRC; 1.

R PROSITE; PSO0119; PROTEIN. KINASE_ATP; 1.

R PROSITE; PSO0107; PROTEIN. KINASE_ATP; 1.

R PROSITE; PSO0109; PROTEIN. KINASE_TYR; 1.

R PROSITE; PSO0109; PROTEIN. KINASE_TYR; 1.

R PROSITE; PSO0109; RECEPTOR_TYR_KIN_V_1; 1.

R PROSITE; PSO0109; PROTEIN KINASE_TYR; 1.

R PROSITE; PSO0109; PROTEIN KINASE, TYR-KIN_V_2; 1.

R PROSITE; PSO0109; PROTEIN KINASE, ATP-binding; Phosphorylation; M Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
                                                                                              SIMILARITY: CONTAINS 1 SAM DONAIN.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
RECEPTOR SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
N-LINKED (GLCNAC. ..) (POTEWTIAL).
N-LINKED (GLCNAC. ..) (POTEWTIAL).
N-LINKED (GLCNAC. ..) (POTEWTIAL).
               SÜBCELLULAR LÒCATION: TYPE I MEMbrane protein.
ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1 (SHOWN HERE) AND 2;
ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: ALMOST EXCLUSIVELY EXPRESSED IN THE NERVOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDZ-BINDING MOTIF (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPHRIN TYPE-A RECEPTOR 5. EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYS-RICH.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY SIMILARITY). (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000561; EGF-like.
InterPro; IPR001090; Ephrin_receptor.
InterPro; IPR000199; Euk_pkinase.
InterPro; IPR0001961; FN_III.
InterPro; IPR0019561; FN_III.repeat.
InterPro; IPR001426; Receptor_tyr_kin_V.
InterPro; IPR001426; Receptor_tyr_kin_V.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF001404; EPH_lbd; 1.
Pfam; PF00061; fn3; 2.
Pfam; PF00061; fn3; 2.
Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ΒY
                                                                                                                                                                                                                                                                                                             EMBL; X95425; CAA64700.1; -.
EMBL; L36644; AAA74245.1; -.
HSSP; P29323; 1B4F.
     tyrosine phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1037
573
594
1037
354
464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             561
1029
1039
1037
707
707
800
650
650
656
2264
369
                                                                                                                                                                                                                                                                                                                                                                 600004;
                                                                                  SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT_SITE
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOD_RES
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BINDING
```

```
N-LINKED (GLCNAC. ..) (POTENTIAL).
LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
SCCECGCGRASSICANAPILIM -> R (IN ISOFORM
                                                                                                                                                     Gaps
                                                                                                                                                      .;
?
                                                                                                                Query Match
43.2%; Score 57; DB 1; Length 1037;
Best Local Similarity 57.9%; Pred. No. 0.97;
Matches 11; Conservative 3; Mismatches 3; Indels
                                                                        1037 AA; 114784 MW; FC2C46C959AFB699 CRC64;
                                                                                                                                                                                                                                                                    Search completed: June 27, 2002, 16:16:52 Job time: 486 sec
                                                                                                                                                                                             594 LSGSCCECGCGRA--SSLC 610
                                                                                                                                                                            LSSSCCKWGCSKSEISSLC 24
423
436
461
619
423
436
461
597
CARBOHYD
CARBOHYD
                            CARBOHYD
                                          VARSPLIC
                                                                        SEQUENCE
SFFFF
                                                                                                                                                                              ò
```

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

June 27, 2002, 16:16:29 ; Search time 58.57 Seconds (without alignments) 70.887 Million cell updates/sec Run on:

US-09-781-077-2_COPY_119_142 132 1 DVLAGLSSSCCKWGCSKSEISSLC 24

Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

562222 Total number of hits satisfying chosen parameters: 562222 seqs, 172994929 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SPTREMBL_19:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_luman:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:* sp_vertebrate:*
sp_unclassified:* sp_organelle:*
sp_phage:*
sp_plant:* sp_rvirus:*
sp_bacteriap:*
sp_archeap:* sp_rodent:* sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Ogdep8 rana escule Ogtrg6.sus scrofa Ogmyk8 felis silve Q28787 papio hamad Q900t9 camelus dro Q2007 mus musculu Q28781 pongo pygma Q9418 drosophila Q9418 arabidopsis Q95yp6 leishmania Q91x78 arabidopsis Q62189 caenorhabdi Q2149 caenorhabdi Q2141 caenorhabdi Q2149 caenorhabdi Q2141 caenorhabdi Q2149 caenorhabdi
	ID	Q9DEP8 Q9TRG6 Q9TRG6 Q2BMYK8 Q28787 Q920G7 Q920G7 Q98181 Q9LV78 Q9LV78 Q9LV78 Q9LV78 Q9LV78 Q9LV78 Q9LV70 Q91L70 Q91L70 Q91L70 Q91L70
	DB	13 6 6 6 6 11 10 5 5 10 10 4
	Query Match Length DB ID	155 122 122 123 123 123 135 1159 1159 1448 169
æ	Query	444 44 44 44 44 44 44 44 44 44 44 44 44
	Score	63 52 52 54 51 51 51 51 51 50 64 69 63
	Result No.	100 100 100 100 100 100 100 100 100 100

035281 mus musculu 035281 mus musculu 098840 mus musculu 098840 mus musculu 095527 drosophila 090wx8 xenopus lae 090x8 xenopus lae 090x8 to arabidopsis 09ytk1 ateline her 02557 homo sapien 015061 homo sapien 034711 paramecium 094431 mus musculu 09443 mus musculu 096498 acropora mi 020896 caenorhabdi 020896 caenorhabdi 095979 crambe abys 090028 capra hircu 099018 dama dama (099x47 galago cras 02323 caenorhabdi 0916759 caenorhabdi 091255 caenorhabdi 091225 caenorhabdis	JENTS	155 AA.	red) sequence update) annotation update)	.a; Vertebrata; Buteleostomi; hia; Ranoidea; Ranidae; Rana.	115SUE-TESTIS; MEDLINE-21309007; PubMed-11416046; MEDLINE-21309007; PubMed-11416046; MEDLINE-21309007; PubMed-11416046; De Rienzo G., Aniello F., Branno M., Minucci S.; "Isolation and characterization of a novel member of the relaxin/insulin family from the testis of the frog Rana esculenta."; Endocrinology 142:3331-3338(2001)	; DB 13; Length 155; . 0.02; tches 6; Indels 0; Gaps 0;	
099119 035281 098718 088840 095527 090908 097181 094711 094711 094711 096718 090806 060718 090802 090802 090802 090802 090802 090802 090802 090802	ALIGNMENT	PRT;	Created) Last sequ Last anno	Craniat Neobatrac	16046; anno M., ton of a ton of a 2001). 2011. IE INSULI IGF_rela 16.	Score 63; DB Pred. No. 0.0 5; Mismatches	5 4 5 5
111 111 111 111 111 111 111 110 6 6 6 6			16, 16,	rog) Nata	Brazat: Brazat: Com 138(2) SEC	, ,	7
272 3627 3672 3672 3672 3673 3673 372 3735 37		PRELIMINARY;	(TrEMBLrel. (TrEMBLrel. (TrEMBLrel. PROTEIN.	Edible fi oa; Chorc hia; Anu	A. : PubMed. haracter: haracter: family fi family fi cocarions BELONGS 729: Insu 052; NG_N 052; NG_N 051: NG_N 052; NG_N 052; NG_N 053; NG_N 054: NG_N 055;	47.78 cy 47.68 ervative	AGLSSSCCKWGCSKSEISSLC : : : AGPALSCCQRGCTKNELMKFC
2000 00 00 00 00 00 00 00 00 00 00 00 00		PREL	(Tre (Tre (Tre PRO	ta (etaz trac 401;	M N.S. 35 37 3007 4 4 4 14 14 14 14 14 14 14 14 14 14 14	larit	KWGC : II
$\begin{array}{c} 44444 \\ 44444444444444444444444444444$		1 DEP8	Q9DEP8; Q1-MAR-2001 (01-MAR-2001 (01-DEC-2001 (RELAXIN-LIKE	insta. Rana esculen Eukaryota; M Amphibia; Ba Acel_TaxID=8	QUENCE FRO SSUE=TESTI DLINE=2130 Rienzo G. Solation al Jaxin/insu/ docrinologi - SIMILAR! BL; AJ2988 HE, AJ2988 FEFPO; IP! TEFPO; IP! TEFPO; IP! ART; SMO001 SSUE; PSO004	Query Match Best Local Similarity 4 Matches 10; Conservati	4 AGLSSSCC : 35 AGPALSCC
118 10000000000000000000000000000000000		SULT DEP8	DT 01 DT 01 DE RE	Ra Ra Ra R	TI TI TI TI TI TI TI TI TI TI TI TI TI T	Query Best L Matche	13
		RES 091 1D	8 E E E E E	80000	R R R R R R R R R R R R R R R R R R R	OME	oy Ob

RESULT Q9TRG6

us-09-781-077-2_copy_119_142.rspt

ö

Gaps

;

```
Camelus dromedarius (Dromedary) (Arabian camel).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
                                                                                                                                                                                                                                                                                                                                                Papio hamadryas (Hamadryas baboon).
Bukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Papio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-20191540; Pubmed=10727251;
Hombach-Klonisch S., Abd-Elnaeim M., Skidmore J.A., Leiser R.,
Fischer B., Klonisch T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Evans B.B.A., Fu P., Tregear G.G.W.;
"Characterisation of primate relaxin genes.";
J. Mol. Endocrinol. 0:0-0(1993).
-:- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
-:- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Ruminant relaxin in the pregnant one-humped camel.";
Biol. Reprod. 62:839-846(2000).
-!- SUBCELLUIAR LOCATION: SECRETED (BY SIMILARITY).
--: SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
EMBL; AF254739; AR67741.1; -.
HSSP; P01348; IRIX.
InterProc. IPRO00739; Insulin_IGF_relaxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.4%; Score 56; DB 6; Length 24;
42.1%; Pred. No. 0.042;
tive 4; Mismatches 7; Indels
                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER 1 1 SEQUENCE 24 AA; 2691 MW; 560BC26A8BADBA14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0cr-2000 (TrEMBLrel. 15, Created)
01-0cr-2000 (TrEMBLrel. 15, Last sequence update)
01-0cr-2001 (TrEMBLrel. 19, Last annotation update)
PREPRORELAXIN.
                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              199 AA.
44.48; Pred. No. 0.21;
                                                                                                                                                                                                      24 AA
                     4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000739; Insulin_IGF_relaxin.
PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00078; IlGF; 1.
PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 LSNKCCHIGCTKKSLAKFC 24
                                                                                    | || || ||: |: ||
163 SDRCCNVGCTRKELADLC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 42.1.
Best Local 8; Conservative
                                                            7 SSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z27106; CAA81622.1;
HSSP; P04090; 6RLX.
                     8; Conservative
                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Camelus dromedarius
                                                                                                                                                                                                                                                                                                           RELAXIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9838;
                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-BABA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09NOT9;
                                                                                                                                                                                                                              028787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9N0T9
                                                                                                                                                                                                          028787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
                                                                                                                                                                   4
                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9T0N60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δŏ
                                                                δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                  Kohsaka T., Takahara H., Sugawara K., Tagami S.; "Endogenous heterogeneity of relaxin and sequence of the major form in pregnant sow ovaries.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Klonisch T., Hombach-Klonisch S., Froehlich C., Kauffold J.,
Steger K., Huppertz B., Fischer B.;
"Nucleic acid sequence of feline preprorelaxin and its localization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Felis silvestris catus (Cat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Felidae, Felis.
                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43.2%; Score 57; DB 6; Length 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

Hombach-Klonisch S., Klonisch T.;

Submitter (FEB-2000) to the EMBL/GenBank/DDBJ databases.

-!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).

-:- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.

EMBL; AF233688; AAF60303.1; --

HSSP; P04090; 6RLX.
                                                                                                                                                                                                                                                                                                                                                                                                                 Piograms (John Hoppe-Seyler 374:203-210(1993).
-!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43.9%; Score 58; DB 6; Length 22; 47.4%; Pred. No. 0.018; tive 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20360 MW; 4C2CF371C698AF9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR000739; Insulin_IGE_relaxin.
PROSITE; PS00262; INSULIN; 1.
SEQUENCE 22 AA; 2527 MW; F4DB254222449313 CRC64;
                                                                                                                                              01-WAY-2000 (TrEMBLrel. 13, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) RELAXIN R-III A CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                      22 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 180 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPR000739; Insulin_IGF_relaxin.
SMART; SM00078; IlGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-00T-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last anno
                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-99115216; PubMed-9915995;
                                                                                                                                                                                                                                                                                                                                   MEDLINE=93257096; PubMed=8489740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   within the feline placenta.";
Biol. Reprod. 60:305-311(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00262; INSULIN; 1. SEQUENCE 180 AA; 20360 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 47.49
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P01348; 1RLX.
                                                                                                                                                                                                                 Sus scrofa (Pig).
                                                                                                                                                                                                                                                                           NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RELAXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART;
                                                                                                             09TRG6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9MYK8
                                                                                      Q9TRG6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               m
```

RESULT Q9MYK8

á a ô

Gaps

; 0

Gaps

ö

8; Indels

6; Mismatches

24

Score 52; DB 6; Length 24; Pred. No. 0.18;

39.48; 33.38;

```
24 AA; 2673 MW; 5615D4B92C1DFD24 CRC64;
                                                                                                                                                                                                                                                           4 AGLSSSCCKWGCSKSEISSLC
                                                                                                                                                        Best_Local Similarity 33.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9600;
                        SEQUENCE
                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     028781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 028781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CG13569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9W1A5
                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
Q9W1A5
                     S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oln X., Miwa T., Aktas H., Gao M., Lee C., Qian Y.M., Morton C.C., Shahsafaei A., Song W.C., Halperin J.A.; Gendic Structure, functional comparison, and tissue distribution of Mamm. Genome 12:82-589(2001).

EMBL; AF292401; AAL04434.1; -.

SEQUENCE 129 AA; 14226 MW; 3B80648C8C30F635 CRC64;
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Gorilla
                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39.8%; Score 52.5; DB 11; Length 129; ilarity 37.5%; Pred. No. 0.8; Conservative 5; Mismatches 4: Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Evans B.B.A., Fu P., Tregear G.G.W.; "Characterisation of primate relaxin genes."; J. Mol. Endocrinol. 0:0-0(1993).

-: SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).

-: SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                   42.4%; Score 56; DB 6; Length 199;
42.1%; Pred. No. 0.34;
tive 5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
199 AA; 22386 MW; F69BBD7E4F4A8089 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79 VAGIQSKCCQWDLCNKNLDGLEEPNNAETSSL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z27228; CAA81742.1; ...
HSSP; P04090; GRLX.
HIGEPPO; IPR000739; Insulin_IGF_relaxin.
PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 LAGLSSSCCKWG-CSK-----SEISSL 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=129/SV;
MEDLINE=21363798; PubMed=11471050;
                                                                                                                                                                                                                                                                             | | ||: |||: |||: |
181 LGERCCQKGCSRKEMATAC 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel, 01, 01-NOV-1996 (TrEMBLrel, 01, 01-DEC-2001 (TrEMBLrel, 19,
                                                                                                                                                                                                                                      6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gorilla gorilla (gorilla).
                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Thes 12; Conserve
                                                                                                                               Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RELAXIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-RG YK;
SEQUENCE
                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q920G7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD59B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                028430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   028430
                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
0920G7
10 095
10 095
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10 097
10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2028430

020401

020401

020401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

030401

03040
g
                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=BERRELEY;
MEDLINE=20196006; PubMed=10731132;
Adama M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Cranlata, Vertebrata, Buteleostoml,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pongo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                       39.4%; Score 52; DB 6; Length 24; 33.3%; Pred. No. 0.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER 1 1 1
SEQUENCE 24 AA; 2673 MW; 5615D4B92C1DFD24 CRC64;
                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9WIA5; TALEMBLEEL. 13, Created) 01-WAY-2000 (TrEMBLEEL. 13, Last sequence update) 01-UNAY-2001 (TrEMBLEEL. 17, Last annotation update) CG13569 PROTEIN.
                                                                                               24 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     868 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Mismatches
                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
            24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00262; INSULIN; 1.
                                                                                                                       01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                              Pongo pygmaeus (Orangutan).
4 SALANKCCHVGCTKRSLARFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 AGLSSSCCKWGCSKSEISSLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 SALANKCCHVGCTKRSLARFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 33.3
Matches 7; Conservative
                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                           RELAXIN (FRAGMENT).
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
```

262 AA; 28098 MW; 5CD397647893BA11 CRC64;

```
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA cherry J.M., Cawley S., Dahlke C., Davenport L.B., Durkov B.C., Dunn P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Durbin K.J., Bryangelista C.C., Ferrac C., Ferriera S., Fleischmann W.,
RA coller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibeywam C.,
RA Humel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
A kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., Moshrefi A.,
RA Markulov G., Milshian N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nakon K., Wurshken D.R., Melson D.L.,
RA Reinert K., Remington K.A., Sannders R.D., Puri V., Reese M.G.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Smith T.,
RA Wang Z.-Y., Wassarman D.A., Welistock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Welistock G.M., Weissenbach J.,
RA Phen X.H., Zhong F.M., Rubin G.M., Venter J.C.,
RA Phen X.H., Zhong F.M., Rubin G.M., Venter J.C.,
RA Phen X.H., Zhong F.M., Rubin G.M., Venter J.C.,
RY The genome sequence of Drosophila melanogaster.",
RY The genome sequence of Drosophila melanogaster.",
RY The genome sequence of Drosophila melanogaster.",
RY Schen H.,
RY Schen B.C., Stapleton M., Stong S., Shu X., Smith R.,
RY H., Ry Schen B.C., Stapleton B.C., Shu X., Shu X., Smith R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence features of the regions of 3,076,755 bp covered by sixty Pl and TAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
GENOMIC DNA, CHROMOSOME 5, P1 CLONE:MXR3.
Arabidopsis thaliana (Mouse-ear Cress).
Bukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eutosides; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TAXID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.0%; Score 51.5; DB 5; Length 868; 52.6%; Pred. No. 7.6; tive 4; Mismatches 4; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           868 AA; 98470 MW; 4EA194B97F240D0E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 262 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20181125; PubMed=10718197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AB019236; BAA97312.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FlyBase; FBgn0034979; CG13569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 SSSCCKWGCSKS-EISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 52.6%
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001283; SCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clones.";
DNA Res. 7:31-63(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00198; SCP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tabata S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9LV78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09LV78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   οχ
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=ATCC 15692 / PAO1;
STRAIN=ATCC 15692 / PAO1;
MEDLINE=20437337; PubMed=10984043;
MEDLINE=20437337; PubMed=10984043;
Stover C. K., Pham X.-C.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Foller K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                   Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                          Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó;
                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-FRIEDLIN;
MEDLINE-98146435; PubMed-9477341;
Troens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M., Smith D.F.;
Query Match 38.6%; Score 51; DB 10; Length 262; Best Local Similarity 47.6%; Pred. No. 2.8; Matches 10; Conservative 4; Mismatches 7; Indels
                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL PREDICTED PROTEIN LM15-1.74, UNKNOWN FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A physical map of the Leishmania major Friedlin genome."; decone Res. 8:135-145(1998).
EMBL; ALIGO371; CAC5905-11; SEQUENCE 370; AA, 38847 MW; 328C7ED7A2174886 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38.6%; Score 51; DB 5; Length 370; 58.8%; Pred. No. 3.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                      370 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1159 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROBABLE TWO-COMPONENT SENSOR.
                                                                                                               121 VLSGLASSLCQWASQVKKHSS 141
                                                                         2 VLAGLSSSCCKWGCSKSEISS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    326 AGHSSSSCKWICRNVQI 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 AGLSSSCCKWGCSKSEI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 58.8
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-FRIEDLIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09HXX0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08 HX 0
                                                                                                                                                                                                                          Q95YP6;
                                                                                                                                                                                                      Q95YP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
                                                                                                                                                                      RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09HYX0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                               В
```

```
Matches
                                                               ολ
                                                                                                            q
                                                                                                                                                                                                                                                        ACCOORDING TO THE STATE OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                   L NATURE 406:959-964(2000).

1 SIMILARITY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.

1 SIMILARITY: TO PROKARYOTE SENSORY TRANSDUCTION PROTEINS.

1 SIMILARITY: TO PROKARYOTE SENSORY TRANSDUCTION PROTEINS.

R INTERPRO: IPRO04359; BCTRLSENSOR.

R INTERPRO: IPRO04359; HS_KIN_SIG.

R INTERPRO: IPRO04561; His_kinA.

INTERPRO: IPRO04361; His_kinA.

INTERPRO: IPRO04361; His_kinA.

INTERPRO: IPRO04361; His_kinA.

INTERPRO: IPRO04361; His_KinA.

INTERPRO: IPRO0441; PAS.

INTERPRO: IPRO0441; PAS.

INTERPRO: IPRO0441; PAS.

INTERPRO: IPRO0441; PAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00387; HATPASSE_C; 1.
SMART; SM00388; HisKA; 1.
SMART; SM00091; PAS; 1.
SMART; SM00448; REC: 1.
PROSITE; PS50283; NA_SOLUT_SYMP_3; 1.
Complete proteome; Kinase; Phosphorylation; Sensory transduction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38.6%; Score 51; DB 16; Length 1159; 35.7%; Pred. No. 12; Live 7; Mismatches 5; Indels 6
  "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1159 AA; 127452 MW; 1C4D145CE0E190CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00001; 7tm_1; 1.
PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
PROSITE; PS00237; G_PROTEIN_RECEP_FI_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_FI_2; 1.
SEQUENCE 399 AA; 45577 MW; 83FP18CF47A7CF88 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           399 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; 281520; CAB04223.1; -.
InterPro; IPR002106; AA_tRNA_ligase_II.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1050 ILAGMNSLLSRWGCQVWTARSREECATL 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VLAGLSSSCCKWGC----SKSEISSL 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                    Pfam; PF02518; HATPase_c; 1.
Pfam; PF00072; response_reg; 1.
Pfam; PF00512; signal; 1.
PRINIS; PR00344; BCTRLSENSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1998 (TrEMBLrel. 07, 01-AUG-1998 (TrEMBLrel. 07, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 35.7;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F31B9.1 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Steward C.A.
"Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F31B9.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      062189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                062189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       none;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           062189
ŏ
```

Length 399;

DB 5; 6.1;

Score 50; Pred. No.

37.9%; 59.1%;

Best Local Similarity

Query Match

```
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
      Gaps
                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Bevan M., Terryn N., Ardiles W., Buysshaert C., Dasseville R.,
De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H.,
      4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.9%; Score 50; DB 5; Length 823; 61.1%; Pred. No. 12;
      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=BRISTOL N2;
Miller N., Bradshaw H., Wu X., Gattung S.;
"The sequence of C. elegans cosmid W03B1.";
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; U58753; AAC24437.1; -. InterPro: IPR002111; Cat_channel_TrpL. Hypothetical protein. SEQUENCE 823 AA; 95286 MW; 5AC484962DCDD7D4 CRC64;
                                                                                                                                                                                                       or-Jun-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 95.3 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
(1-4)-BERR-MANNAN ENDOHYDROLASE-LIKE PROTEIN.
      4;
                                                                                                                                                                             823 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  448 AA
  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
                                                          343 DVAAGISSFCC-WLLPSFSKSE 363
                                      1 DVLAGLSSSCCKW---GCSKSE 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   664 LTSGCCK--CSSTAISSL 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 LSSSCCKWGCSKSEISSL 23
13; Conservative
                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waterston R.;
"Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                       Q23141
Q23141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9LZV3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9LZV3
                                                                                                                                   RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                       023141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9LZV3
```

```
RA Villaroel R., Gielen J., Van Montagu M., Bancroft I., Mewes H.W.,
RA Rudd S., Lemcke K., Mayer K.F.X.;
RI Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RA EDGUENCE FROM N.A.
RA EDGUENCE FROM N.A.
B. DATABIGOPSIS sequencing project;
R. Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
B. ELATABICASIS.1. - CAB82761. - CAB
```

```
June 27, 2002, 16:08:08; Search time 73:16 Seconds (without alignments) 40.992 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                               1 RAAPYGVRLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                             747574 seqs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                     OM protein - protein search, using sw model
                                                                                                                                                                                  US-09-781-077-2_COPY_26_52
150
                                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A_Geneseq_032802:*
                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                          Perfect score:
                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database :
                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                              Run on:
```

| SIDSI/gggdata/hold geneseq/geneseqp-embl/AA1990.bar; |
| SIDSI/gggdata/hold geneseq/geneseqp-embl/AA1990.bar; |
| SIDSI/gggdata/hold geneseq/geneseqp-embl/AA1991.bar; |
| SIDSI/gggdata/hold geneseq/geneseqp-embl/AA1991.bar; |
| SIDSI/gggdata/hold geneseq/geneseqp-embl/AA1991.bar; |
| SIDSI/gggdata/hold-geneseq/geneseqp-embl/AA1992.bar; |
| SIDSI/gggdata/hold-geneseq/geneseqp-embl/AA1994.bar; |
| SIDSI/gggdata/hold-geneseq/geneseqp-embl/AA1995.bar; |
| SIDSI/gggdata/hold-geneseq/geneseqp-embl/AA1996.bar; |
| SIDSI/gggdata/hold-geneseq/geneseqp-embl/AA1996.bar; |
| SIDSI/gggdata/hold-geneseq/geneseqp-embl/AA1999.bar; |
| SIDSI/gggdata/hold-geneseq/geneseqp-embl/AA1999.bar; |
| SIDSI/gggdata/hold-geneseq/geneseqp-embl/AA1999.bar; |
| SIDSI/gggdata/hold-geneseq/geneseqp-embl/AA2000.bar; | /SIDSI/gogdata/hold-geneseg/genesegp-embl/AA1980.DAT:*
/SIDSI/gogdata/hold-geneseg/genesegp-embl/AA1981.DAT:*
/SIDSI/gogdata/hold-genesegp-embl/AA1981.DAT:*
/SIDSI/gogdata/hold-genesegp-embl/AA1983.DAT:*
/SIDSI/gogdata/hold-geneseg/genesegp-embl/AA1984.DAT:*
/SIDSI/gogdata/hold-geneseg/genesegp-embl/AA1984.DAT:*
/SIDSI/gogdata/hold-geneseg/genesegp-embl/AA1986.DAT:*
/SIDSI/gogdata/hold-geneseg/genesegp-embl/AA1987.DAT:*
/SIDSI/gogdata/hold-geneseg/genesegp-embl/AA1987.DAT:*
/SIDSI/gogdata/hold-geneseg/genesegp-embl/AA1987.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Human insulin homo Asymmetry sequence Insulin-like pepti Human zins3 B chai Human Zins3 protei Pro-insulin-like p PRO182 polypeptide Human PRO182 prote Human Insulin fami PRO182 Polypeptide Human EST encoded
SUMMARIES	AAG78114 AAR96006 AAY91963 AAY91963 AAW37925 AAW31925 AAW31913 AAB2431 AAB2433 AAY83228 AAX83228
% Query Match Length DB	142 40 172 30 20 30 20 31 21 135 19 135 21 135 21 135 21 135 21 135 21 135 21
Query Match L	1000.0 58.0 58.0 54.7 54.7 54.7 54.7 54.7 7.45 7.45 7.45
Score	150 822 822 822 823 823 823 824 825
Result No.	1 2 2 4 3 4 4 7 6 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

Human PRO182 polyp Human immunostimul Human anglogenesis Relaxin-like facto Mouse Zins3 protei	Human RIf partial Prorelaxin B-chain Human relaxin B-ch Ubiquitin C-termin Ubiquitin-relaxin HZ prorelaxin qene HZ prorelaxin dedu	Sequence of human Sequence of human Sequence of human Amino acid sequenc Amino acid sequenc Angiotensin conver Asymmetry sequence Relaxin analogue B	Human relaxin part Relaxin B-chain. Sequence of porcin Human secreted pro Human gene 2 encod Caenorhabditis ele C. elegans insulin Human gene 2 encod Human gene 2 encod Proliciarin fragme	Rat Zins2 testis-s
AAU12309 AAB20110 AAB53072 AAW07863 AAW37926 AAW35771		444	AABUO1/ AAR6490 AAP40156 AAY8706 AAE0604 AAB06114 AAX8715 AAX8715 AAE0613 AAC033A	AAW475
			22122122122122122222222222222222222222	
135 135 135 135 135	2224 1111 10020	1855 1855 1855 1855 2055 2057	40 182 182 182 182 106 106 1150 1150	188
	01111111	·	2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	
82 82 76 75	74 71 71 71 71 71	71 71 71 71 71 69 68	> \QUUUUUUUU\QUU\Q\\\\\\\\\\\\\\\\\\\\\\	53
12 13 14 15 16		3 3 3 5 5 5 6 7 6 7 6 7 6 7 6 7 6 7 6 7 6 7 6	3 4 5 9 8 8 8 9 8 9 8 9 8 9 9 9 9 9 9 9 9 9	45

ALIGNMENTS

SUL G78	2 AAG78114;	r 21-NOV-2001 (first entry)	Human insulin homologue polypeptide Zins4.	Human; insulin; zins4; relaxin; chromosome 19p13.11; cytostatic; antifertility: vasofronic: reproductive disordar, property as a feet of the control of the					Homo sapiens.	No.N		•	Protein	/label=	`	Region 2652	/label-	/note= "Claimed in claim 1" Region 34 47		/voc. p_nath_consense_sequence_region /note= @1ven in SEO ID NO 3"	Region	/label= B_chain_conserved_motif
. AAAC	X X	TQ X	X	KW W	ΚW	K K	ΚW	X X	SO	X X	F	FT	FŢ	FT	FT	E E	FI	FT	FT	FT	FŢ	FT

/note= "Given in SEQ ID NO 5"

/note= "Cleavage site at the junction of the C peptis and the A chain with a conserved RXXR motif"

55..114 /note= "Claimed in claim 3"

.118

/label= C_peptide

/label= A_chain_consensus_sequence_region /note= "Given in SEQ ID NO 4"

/label= A_chain /note= "Claimed in claim 2"

119..142

.142

```
09-FEB-2001; 2001WO-US04199.
                                      10-MAR-2000; 2000US-0523346
                           WO200168862-Al
 Cleavage-site
          Cleavage-site
                                                                                                                     Sequence
       Region
               Region
                     Region
   Region
```

```
The invention relates to an isolated insulin homologue zinst having chomology to the relaxin family. The zinst gene, located on chromosome homology to the relaxin family. The zinst gene, located on chromosome 19p13.11, encodes a 142 amino acid protein, where the Linst polyperlide comprises a B chain and A chain comprising amino acid residues 26.52 and comprises a B chain and A chain comprising amino acid residues 26.52 and 119-142 respectively, joined by inter- and intra-chain disulfide bonds. Cinst has cytostatic, antifertility and vasotropic activity. Zinst protein is an animals and in therapies for treating resisted reproductive disorders. Zinst protein is useful in treating reproductive, comprise to kits activity. Zinst protein is useful in treating reproductive, combinators of its activity. Zinst polypeptides and modulators of the cinhibitors of its activity. Zinst polypeptides and modulators of the compression of its activity. Zinst polypeptides and modulators of the compression of compression conditions in overy. Poetcetion of zinst functions including patchlogical conditions in overy. Poetcetion of zinst polypeptides in the serum or tissue biopsy of a patient is useful for diagnosing ovarian cancer. The molecules are also useful for treating dysfunction associated with contractile tissues or to suppress or enhance contractility in vitro fertilization, control, treating importace or other male reproductive dysfunction, inducing birth, for promoting growth, differentiation, development and/or maturation of ovarian cells, myocytes, endothelial cells, osteoblasts in colluctive and in the study of the ovarian oyle, reproductive directions and fertilization. The polypeptide is also useful as a modulator of blood pressure, muscle tension and osmotic cuseful as a modulator of blood pressure, muscle tension and osmotic
                                                                                                                                                                                                                                                                                                                                                                            New insulin homologue polypeptide having homology to relaxin family, designated zins4 and zins4 polynucleotide, useful for diagnosing, preventing, treating reproductive, prostate, heart and kidney disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; Page 72-73; 79pp; English.
                                                                                                       Holloway JL, Lok S, Jaspers SR;
(ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                          WPI; 2001-582454/65.
                                                                                                                                                                                                                                                                                       N-PSDB; AAH79088
```

```
AAR AAR95999-R96006 represent the asymmetry sequences of target binding assemblies (TBA) of the invention. The TBA is recognised by the target binding region (TBR) of a probe of the invention. The probe of the total binding region (TBR) of a probe of the invention. The probe of the invention contains at TBR, a booster binding region (BBR), and an optional support or attachment (OSA). The TBA contains at least one uncleic acid recognition unit (NAR), and optionally a linker sequence, an asymmetry sequence, an unclear localisation signal ascenbly sequence, and an OSA. The assembly sequence and asymmetry sequences are responsible for the folding and association of the NARs. The NARs are responsible for the folding and association of the NARs. The NARs are responsible for the folding and association of the Dahllomavirus (HPV) LTR and Tat binding units. The LINKer sequence is an oligopeptide, which does not interfere with NAR inter sequence is an oligopeptide, which does not interfere with NAR function, but provides stability and control over the spacing of the NAR interfere means of localisation of the probe. The probe can be used in a method for detecting or localising a specific target nucleic acid containing systems, including bacteria and viruses.
                                                                                                                                                                                                                                                                                   Target binding assembly; nucleic acid recognition unit; NF-kappa-B; SP1; TATA; human papillomavirus; HPV; HPV E2; human immunodeficiency virus; HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence; nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probe nucleic acids, target binding assemblies, etc - for detection and localisation of specific nucleic acid sequences, esp. HIV and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 21; Page 108-109; 172pp; English.
                  26 raapygvrlcgrefiraviftcggsrw 52
27
                                                                                                                                   AAR96006 standard; peptide; 40 AA.
  1 RAAPYGVRLCGREFIRAVIFTCGGSRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94US-0353476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Weininger S;
                                                                                                                                                                                                                  19-FEB-1997 (first entry)
                                                                                                                                                                                                                                                         Asymmetry sequence #8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENE-) GENE POOL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1996-287199/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 40 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Weininger AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09617956-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                            AAR96006;
                                                                                                   N
                                                                                                                     AAR96006
                                                                                                                                                                                g
```

Gaps

. 0

Query Match
Best Local Similarity 100.0%; Score 150; DB 22; Length 142;
Best Local Similarity 100.0%; Pred. No. 6.3e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0;

Conservative

Best Local Similarity
Matches 14; Conserv

Query Match

Gaps

; 0

58.0%; Score 87; DB 17; Length 40; 70.0%; Pred. No. 1.9e-05; tive 3; Mismatches 3; Indels

RESULT

g

```
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW37925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
             The present sequence represents insulin-like polypeptide (pro-ILP)
chain B peptide. The ILP protein is expressed in the colon and uterus,
and is a member of the insulin/IGF family. The immature pro-ILP
comprises a 135 amino acid sequence, which is processed into the mature
comprises a 135 amino acid sequence, which is processed into the mature
form which comprises an A chain and a B chain linked by disulfide bonds.
The C-peptide of pro-ILP saists as a separate peptide after processing
of pro-ILP. The ILP protein is useful in treatment of disorders related
to neurophysiological function affecting fluid homeostasis, electrolyte
concortais, cardiavosacular function, blood pressure, somatic or cardiac
homeostasis, cardiavosacular function, blood pressure, somatic or cardiac
lonotropic activity, cardiac chronorropic activity and collagen
conficien of the uterus, colon or other ILP-expressing cell
or tissue and for diagnosis and screening of modulators and therapeutics.

The process of the color of appear in the specification; it was
                                                                                                                                                                                                                                                          Insulin-like polypeptide; pro-ILD; ILD; insulin/IGF family; A chain; B chain; C chain; neurophysiological function; fluid homeostasis; electrolyte homeostasis; cardiovascular function; blood pressure; somatic; cardiac ionotropic activity; cardiac chronotropic activity; collagen deposition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Colon and uterus expressed insulin-like polypeptide, useful in the treatment of disorders related to neurophysiological function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54.7%; Score 82; DB 20; Length 30;
66.7%; Pred. No. 7.5e-05;
Live 2; Mismatches 5; Indels
                                                                                                                                                                                                                       Insulin-like peptide (pro-ILP) chain B peptide.
                                                                                                          AAY01963 standard; Peptide; 30 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; Page -; 75pp; English.
9 rlcgrdlirafiylcggtrw 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 vrlcgleyirtviyicassrw 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 VRLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0059836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-US17888
                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 66.7
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-254713/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAX35207
                                                                                                                                                                                     01-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1999.
                                                                                                                                                AAY01963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gurney A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
AAY95773
ID AAY99
                                                                                            AAY01963
```

```
Identifying mutations in human chromosome 1p31, preferably a zins3 gene mutation, comprises using an insulin/relaxin family member (designated zins3), useful for diagnosing non-insulin dependent diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is that of a peptide from the B chain of human zin3 (see AAY9570). The peptide was used to immunize guinea Pigs, rabbits and chickens to generate antibodies for zins3, which were used in assays to determine the tissue distribution and cell expression of zins3. Zins3 is a novel member of the insulin/relaxin family whose gene maps to a region of human chromosome ip associated with non-insulin dependent diabetes mellitus (NIDDM). Zins3 polynuclectides and polypeptides can be used to diagnose disorders associated with abnormal expression of zins3 and to identify polymorphisms that result from mutations in the zins3 gene. The invention provides methods for identifying abnormalities in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression that are a factor in causing, or predisposing, a person to some defect in glucose metabolism, such as NIDDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insulin homologue; identification; isolation; Zins3 receptor; treatment; disease; pre-elampsia; premature labour; Human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54.7%; Score 82; DB 21; Length 31; 66.7%; Pred. No. 7.8e-05; Live 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jaspers SR, Whitmore TE, Conklin DC, Lofton-Day CE,
                                                                                                                                                         Zins3; insulin; relaxin; human; diagnosis; NIIDM; non-insulin dependent diabetes mellitus; immunogen.
                                                                                                       Human zins3 B chain peptide immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW37925 standard; Protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 5; Page 34; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 vrlcgleyirtviyicassrw 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 VRLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0250125.
                                                                                                                                                                                                                                                                                                                                                                                                              10-FEB-2000; 2000WO-US03515.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0198248
                                                 07-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 66.7 nes 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-558220/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Zins3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 AA;
                                                                                                                                                                                                                                                                                                   WO200047776-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-FEB-1999;
                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                       17-AUG-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
AAY95773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW37925;
```

ö

AAY95773 standard; Peptide; 31 AA.

δλ qq

```
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB00173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Zins3 protein is an insulin homologue protein. Polynucleotide molecules taken from its gene can be introduced into a cultured cell using an expression vector. The cell will express an insulin homologue polypeptide encoded by the polynucleotide. The polypeptides can also be expressed by introducing the polynucleotides into the germline of a nonhuman animal. The polypeptides can be used to identify and isolate receptors for zins3. Antibodies and antagonists of the polypeptides can be used for treating disease associated with extracellular matrix and vessels. The antibodies may also be used in the diagnosis of diseases associated with the polypeptide, such as reproductive diseases associated with the placenta and uterus, gastrointestinal diseases, and placental and colon pathology. Antagonists against the polypeptide may also be used to treat diseases such as preclampsia, premature labour, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insulin-like polypeptide; pro-ILP; ILP; insulin/IGF family; A chain; B chain; C chain; neurophysiological function; fluid homeostasis; electrolyte homeostasis; cardiovascular function; blood pressure; somatic; cardiac ionotropic activity; cardiac chronotropic activity; collagen deposition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                           Insulin homologue polypeptide(s) and antagonists – used to, e.g. treat pre-eclampsia, premature labour and Crohn's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 82; DB 19; Length 135;
Pred. No. 0.00034;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                   Jaspers SR, Lofton-Day CE, Lok S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pro-insulin-like peptide (pro-ILP).
                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY01961 standard; Protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 64-65; 81pp; English.
                                                                           "C-peptide"
                                            "B chain"
                                                                                                         /note= "A chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 vrlcgleyirtviyicassrw 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 VRLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.7%;
                                                                                                                                                                                                      97WO-US18593
                                                                                                                                                                                                                                      96US-0028177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 66.7%
                                                                             /note= "C-
115..135
                                                                                                                                                                                                                                                                   (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                WPI; 1998-251285/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135 AA;
                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAV29150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Crohn's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-1999
                                                                                                                                           WO9816635-A1
                                                                                                                                                                                                                                      15-OCT-1996;
                                                                                                                                                                                                        15-OCT-1997;
                                                                                                                                                                                                                                                                                                    Conklin DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                               Peptide
                                                              Peptide
                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY01961
```

ŏ

```
The present sequence represents an insulin-like polypeptide (pro-ILP). The protein is expressed in the colon and uterus, and is a member of the insulin/IGF family. The immature pro-ILP comprises a 135 amino acid sequence, which is processed into the mature form which comprises an A chain and a B chain linked by disulfide bonds. The C-peptide of pro-ILP exists as a separate peptide after processing of pro-ILP. The ILP protein is useful in treatment of disorders related to neurophysiological function affecting fluid homeostasis, electrolyte homeostasis, cardiovascular function, blood pressure, somatic or cardiac homotropic activity, cardiac chronotropic activity and collagen deposition. The methods can be used for diagnosing a physiologic or pathologic condition of the uterus, colon or other ILP-expressing cell or tissue and for diagnosis and screening of modulators and therapeutics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRO211; PRO228; PRO538; PRO172; PRO182; neoplasia; inhibition; tumour; treatment; therapy; agonist; antibody; breast cancer; vovarian cancer; renal cancer; colorectal cancer; uterine cancer; prostate cancer; lung cancer; bladder cancer; melanoma; leukaemia; inflammatory disorder; angiogenic disorder; immunologic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Colon and uterus expressed insulin-like polypeptide, useful in the treatment of disorders related to neurophysiological function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 82; DB 20; Length 135;
Pred. No. 0.00034;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52..58
/note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1..18
/label= Signal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB00173 standard; Protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 5; Fig 6B; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 VRLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 vrlcgleyirtviyicassrw 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54.7%;
66.7%;
                                                                                                                      98WO-US17888.
                                                                                                                                                                                      97US-0059836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.7*
Matches 14; Conservative
                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-254713/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRO182 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAX35204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
WO9915664-A1
                                                                                                                         28-AUG-1998;
                                                                                                                                                                                      24-SEP-1997;
                                                            01-APR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB00173;
                                                                                                                                                                                                                                                                                                                           Gurney A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence
```

ö

```
Isolated PRO211, PRO228, PRO538, PRO172 or PRO182 polypeptides

or their agonists (preferably anti-PRO agonist antibody or a small
molecule minicking the biological activity of PRO polypeptide) are
useful in vitro or in vivo for inhibiting the growth of a tumour cell.

Compositions comprising the PRO polypeptides are useful for
inhibiting neoplastic cell growth and for treating cancer including
breast, ovarian, renal, colorectal, uterine, prostate, lung, bladder,
central nervous system cancer, melanoma and leukemia in a mammal.
The PRO POLYPeptides are also useful for treating other disorders
such as neuronal, glial, astrocytal, hypothalamic and other glandular,
inflammatory, anglogenic and immunologic disorders and
inflammatory, anglogenic and immunologic disorders as well as being
useful for identifying agonists to PRO polypeptides by contacting the
polypeptide with a candidate molecule and monitoring biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ashkenazi AJ, Goddard A, Gurney AL, Klein RD, Napier MA, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRO211, PRO228, PRO538, PRO172 and PRO182 polypeptides useful for treating tumors including cancers of the breast and lung, leukeamia and for identifying compounds capable of inhibiting growth of neoplastic cells
                                                                   /note= "cAMP- and cGMP-dependent protein kinase 113\dots117
                                                                                                      /note= "Casein kinase II phosphorylation site"
              /note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                           /note= "Casein kinase II phosphorylation site"
                                                                                                      121...136 // Label Insulin family signature 125...131
                             96..102
/note= "N-myristoylation site"
                                                                                                                                                       /note= "N-myristoylation site"
127..131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 31; Fig 10; 133pp; English.
                                                                                                                                                                                                                                                                                                                                                                            99WO-US20594.
99WO-US21090.
99WO-US23089.
                                                                                                                                                                                                                                                                                                                                               99US-0144758.
99US-0145698.
                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US28313.
                                                                                                                                                                                                                                                                                     99WO-US28564
                                                                                                                                                                                                                                                                                                                 99US-0123957
                                                          ..111
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-638201/61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAA54109
                                                                                                                                                                                                                         WO200055319-A1
 Modified-site
                                                        Modified-site
                                                                                     Modified-site
                                                                                                                                                 Modified-site
                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                              20-JUL-1999;
26-JUL-1999;
08-SEP-1999;
                                                                                                                                                                                                                                                                                   02-DEC-1999;
                                                                                                                                                                                                                                                       21-SEP-2000.
                                                                                                                                                                                                                                                                                                                 12-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                          15-SEP-1999;
05-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                        30-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (uan J;
```

```
ó
                                            Gaps
                                          ô
 54.7%; Score 82; DB 21; Length 135; 66.7%; Pred. No. 0.00034; Live 2; Mismatches 5; Indels
Query Match
Best Local Similarity 66.7'
Matches 14; Conservative
```

useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorder in mammals by modulating cell proliferation, angiogenesis and cardiovascularisation, and for identifying agonists and antagonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PRO expression such as cardiovascular, endothelial or angiogenic disorders in mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors containing them and the PRO polypeptide may be used to treat disorders associated with decreased PRO expression. AAA77510 to AAA77721 and AAB24388 to AAB2435 represent nucleotide and protein sequences used in the exemplification of the present invention.

135 AA;

Sequence

The present invention describes nucleic acids encoding PRO polypeptides

```
26 vrlcgleyirtviyicassrw 46
7 VRLCGREFIRAVIFTCGGSRW 27
```

셤 δ

```
diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy; angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic; cytostatic; gene therapy; vaccine.
                                                                                 Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
                                                                                                                                                                                                                                                                                                                                                                                                       Goddard A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorders in mammals.
                                                                                                                                                                                                                                                                                                                                                                                                     Baker KP, Ferrara N, Gerber H, Hillan KJ, Goddi
Gurney AL, Klein RD, Kuo SS, Paoni NF, Smith V;
Williams PM, Wood WI;
                                                              Human PRO182 protein sequence SEQ ID NO:16.
       AAB24391 standard; Protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 72; Fig 8; 315pp; English.
                                                                                                                                                                                                                                                                                                                                     99WO-US21090.
99WO-US21547.
99WO-US23089.
                                                                                                                                                                                                                                                                       99WO-US12252.
99US-0141037.
                                                                                                                                                                                     99WO-US28313
                                                                                                                                                                                                                                                    99US-0131445.
                                                                                                                                                                                                                                                                                                         99WO-US20111.
                                                                                                                                                                                                                                 99WO-US05028
99US-0123957
                                                                                                                                                                                                                                                                                        99US-0144758
                                                                                                                                                                                                                                                                                                                             99WO-US20944
                                                                                                                                                                                                                                                                                                                                                                99US-0162506
                                                                                                                                                                                                                                                                                                                                                                                                                       Williams PM,
                                            07-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                   (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-412154/35.
N-PSDB; AAA77521.
                                                                                                                                               WO200032221-A2.
                                                                                                                                                                                                                                                                                                                                                                                                   Ashkenazi AJ,
                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                             Godowski PJ,
Watanabe CK,
                                                                                                                                                                                    30-NOV-1999;
                                                                                                                                                                   08-JUN-2000.
                                                                                                                                                                                                                                                    28-APR-1999
14-MAY-1999
                                                                                                                                                                                                                                                                      02-JUN-1999
                                                                                                                                                                                                                                                                                                                   08-SEP-1999
                                                                                                                                                                                                                                                                                                                                               15-SEP-1999
                                                                                                                                                                                                                                                                                                          01-SEP-1999
                           AAB24391;
AAB24391
```

ò

ö

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      insulin/relaxin family. The zins3 gene maps to human chromosome insulin/relaxin family. The zins3 gene maps to human chromosome pall, a region that is correlated to a heritable form of non-insulin dependent diabetes mellitus (NIDDM). zins3 mRNA is not expressed in detectable amnounts in healthy tissue, indicating that the zins3 copynucleotide is a candidate marker for a disease state and/or a specialized cell type. zins3 polynucleotides and polypeptides can be used to diagnose disorders associated with abnormal expression of the zins3 protein, and to identify polymorphisms that result from mutations in the zins3 gene. In particular, the invention provides methods for identifying abnormalities in expression that are a factor in causing, or predisposing, a person to some defect in quicose metabolism, such as NIDDM. Processing of the mature zins3 protein involves cleavage at the C-terminus of the signal peptide and, based on predicted structural homology with other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying mutations in human chromosome 1p31, preferably a zins3 gene mutation, comprises using an insulin/relaxin family member (designated zins3), useful for diagnosing non-insulin dependent diabetes
                                                                   Gaps
                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lok S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of zins3, a novel member of the
54.7%; Score 82; DB 21; Length 135; 66.7%; Pred. No. 0.00034; Live 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jaspers SR, Whitmore TE, Conklin DC, Lofton-Day CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zins3; insulin; relaxin; human; diagnosis; NIIDM;
non-insulin dependent diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..22
'label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human insulin family homologue zins3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Page 44-45; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                   AAY95770 standard; Protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23..48
/label= B-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= C-chain
115..135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115..135
/label= A-chain
                                                                                                                                 7 VRLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                    |||||| |:|| ||: | |||
26 vrlcgleyirtviyicassrw 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0198248.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-FEB-2000; 2000WO-US03515.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0250125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                   14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-558220/51.
                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAA50150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200047776-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-FEB-1999;
12-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                             AAY95770;
            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                         σ
                                                                       Matches
                                                                                                                                                                                                                                                                                                                  AAY95770
                                                                                                                                                                                                                                                                                         RESULT
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ashkenazi A, Goddard A, Gurney AL, Klein RD, Napier M, Wood WI;
                                                                                                                                                                                                                                                                                                                                                        Inhibition; cancer; neoplasia; tumour; breast; ovary; renal; colorectal; uterus; prostate; lung; bladder; central nervous system; CNS; melanoma; leukaemia; PRO211; PRO228; PRO538; PRO172; PRO182;
members of the insulin family, cleavage at the C-terminus of the B-chain and at the N-terminus of the A-chain, resulting in removal of the C-peptide. Cysteine residues at positions 29 and 41 (B-chain) and 121 and 135 (A-chain) are capable of associating through cysteine bridges and forming disulfide-bonded molecules.
                                                                                                                                           ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "cAMP and cGMP dependent protein kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Casein kinase II phosphorylation site"
                                                                                                                54.7%; Score 82; DB 21; Length 135; 66.7%; Pred. No. 0.00034;
Live 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Insulin family signature sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "N-myristoylation site"
52..58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /...102
/note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                          AAY83228 standard; Protein; 135 AA
                                                                                                                                                                                   |||||| |:|| ||: | |||| || 26 vrlcgleyirtviyicassrw 46
                                                                                                                                                                     7 VRLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0104080.
                                                                                                                                                                                                                                                                                                             16-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ...131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ...131
                                                                                                                                Best Local Similarity 66.7
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113..117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .102
/note= "
107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88..92
/note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-317943/27.
                                                                                                                                                                                                                                                                                                                                    PRO182 Polypeptide.
                                                                                135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAZ93704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200021996-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-APR-2000
                                                                                Sequence
                                                                                                                                                                                                                                                                                     AAY83228;
                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                                                                                                                                                    human.
                                                                                                                                                                                                                                    RESULT 10
                                                                                                                                                                                                                                               AAY83228
                                                                                                                                                                                                                                                                                     qq
      88888888
```

Gaps

. 0

54.7%; Score 82; DB 22; Length 135; 66.7%; Pred. No. 0.00034; 1ive 2; Mismatches 5; Indels

27

|||||| |:|| ||: | ||| 26 vrlcgleyirtviyicassrw 46

7 VRLCGREFIRAVIFTCGGSRW

Query Match
Best Local Similarity 66.74

protein of the invention.

135 AA;

Sequence

```
SXS
                                                                                                                                                                                      Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomator. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides the protein and coding sequences of novel
             Composition for inhibiting neoplastic cell growth and treating cancers of ovary, uterus, prostate, lung and bladder, comprises PRO211, PRO228, PRO538, PRO172 or PRO182 polypeptide or their agonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use -
                                                                                                                                polypeptide or their agonists, mixed with a carrier is useful for inhibiting neoplastic growth and treating tumnors such as cancers of breast, ovary, renal, colorectal, uterus, prostate, lung, bladder, central nervous system, melanoma and leukaemia.
                                                                                                             Compositions comprising a PRO211, PRO228, PRO538, PRO172 or PRO182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                               54.7%; Score 82; DB 21; Length 135; 66.7%; Pred. No. 0.00034; Live 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; Page 1068-1069; 1275pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human EST encoded protein SEQ ID NO: 1558.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cao Y, Drmanac RA, Zhang J, Werhman T;
                                                                              Claim 14; Figure 10; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM24033 standard; Protein; 135 AA
                                                                                                                                                                                                                                                                                                                                                26 vrlcgleyirtviyicassrw 46
                                                                                                                                                                                                                                                                                                                               7 VRLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JAN-2000; 2000US-0491404.
17-JUL-2000; 2000US-0617746.
03-AUG-2000; 2000US-0631451.
15-SEP-2000; 2000US-0663870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JAN-2001; 2001WO-US02687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                              14; Conservative
                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-476164/51.
                                                                                                                                                                                                                Sequence 135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAH98692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200154477-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM24033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                              AAM24033
ŏ
```

```
Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate, cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gao W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Beresini M, Deforge L, Desnoyers L, Filvaroff E, G;
ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
AAU12309 standard; Protein; 135 AA.
                                                                     Human PRO182 polypeptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                11 - FEB - 2000; 2000MO-USOUS 565.

18 - FEB - 2000; 2000MO-USOUS 565.

18 - FEB - 2000; 2000MO-USOUS 434.

24 - FEB - 2000; 2000MO-USOL 414.

24 - FEB - 2000; 2000MO-USOL 414.

24 - FEB - 2000; 2000MO-USOL 601.

20 - MAR - 2000; 2000MO-USOL 501.

21 - MAR - 2000; 2000MO-USOL 537.

21 - MAR - 2000; 2000MO-USOL 537.

22 - MAY - 2000; 2000MO-USUS 439.

17 - MAY - 2000; 2000MO-USUS 430.

30 - MAY - 2000; 2000MO-USUS 430.
                                                                                                                                                                                                                                01-DEC-2000; 2000WO-US32678.
                                                                                                                                                                                                                                                                                                                                          99WO-US30911,
                                                                                                                                                                                                                                                                                                                                                                  99WO-US31243,
2000WO-US00277,
                                                                                                                                                                                                                                                                                                                   99US-0170262
99WO-US30095
                                                                                                                                                                                                                                                                                                       99WO-US28565
                                             24-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stewart TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-408281/43.
                                                                                                                                                                                WO200140466-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAS21381
                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gerritsen ME,
                                                                                                                                                                                                                                                                                        02-DEC-1999;
02-DEC-1999;
09-DEC-1999;
16-DEC-1999;
20-DEC-1999;
30-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000;
02-JUN-2000;
                                                                                                                                                                                                        07-JUN-2001.
                        AAU12309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith V,
```

```
AAU12172-AAU12446 represent novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartlage, the proliferation of inner ear unficular supporting cells or of T-lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells Some of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                    the PRO polypeptides may modulate glucose or free fatty acid uptake by skelteral muscle cells or by adipocytes, or inhibit binding of A-peptide to factor VITA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polynucleotides encoding
        Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammallan tumours e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "cAMP- and cGMP-dependent protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRO182; UNQ156; human; immune disease; autoimmune disease; antirheumatic; antiarthritic; antiinflammatory; antianaemic; immunosuppressive; antithyroid; antidlabetic; neuroprotective; hepatotropic; virucide; dermatological; antipsoriatic; antiallergic; immunostimulant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54.7%; Score 82; DB 22; Length 135; 66.7%; Pred. No. 0.00034; ive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96..102
/note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label- Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19..135
/label= Mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB20110 standard; Protein; 135 AA.
                                                                                                               Claim 12; Fig 276; 813pp; English.
                                                                         lung, breast, prostate, cervical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||||| |:|| ||: | |||
26 vrlcgleyirtviyicassrw 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 VRLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunostimulant PRO182.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 66.7
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52..58
/note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB20110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB20110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
```

```
The present sequence is that of PRO182 (UNQ156), a novel human continuous protein encoded by cDNA (see AAF30052) isolated immunomodulator protein encoded by cDNA (see AAF30052) isolated from a uterine cDNA library. The invention provides Polynucleotides (see AAF30050-62) encoding novel human PRO proteins (see AAB20108-20) including PRO182. Claimed composition of inflammatory cells into a tissue of a mammal, stimulating or enhancing an immune cesponse in a mammal, or increasing the proliferation of T-lymphocytes in a mammal in response to an antigon. Claimed compositions comprising the PRO polypeptide or its antagonist have the opposite of effect. A claimed method for treating an immune related disorder, involves administating the PRO polypeptide, comprising the PRO polypeptide or its antagonist have the opposite or selected from systemic lupus erythematosus, rheumatoid arthritis, consist antibody or an antagonist antibody. The disorder is selected from systemic lupus erythematosus, rheumatoid arthritis, costeoarthritis, juvenile chronic arthritis, spoodyloarthropathy, systemic vasculitis, sarcoldosis, autoimmune haemologic of systemic vasculitis, sarcoldosis, autoimmune haemologic autoimmune heamboy, pagentis, selecteds multiple sclerosis, autoimmune chromboytopeania, thyroiditis, diabetes mellitus, inflammatory bowel disease (uncommune colitis and cornin antiple sclerosis), autoimmune chromboytopeania, thyroiditis, diabetes mellitus, billiary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, billiary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, altoimmune mediated skeases (such as bullous skin disease, (auto)immune mediated cornin and graft-vascus colated diseases (such as graft rejection and graft-vascus-host disease, cirther as graft rejection and graft-vascus-host disease, cirther and compound capable of inhibiting the expression of the PRO polypeptide, vectors, host cells and compound capable of inhibiting the arression or the level of expression of the PRO sponsitivity of the PRO 
                                                                                                                                                                                                                                                                                                              Godowski PJ, Gurney AL;
Tumas D, Watanabe CK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        New PRO polypeptides, nucleic acids and (ant)agonists, useful for diagnosing and treating immune-related disorders, such as multiple sclerosis, rheumatoid arthritis and diabetes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.7%; Score 82; DB 22; Length 135; 66.7%; Pred. No. 0.00034; Live 2; Mismatches 5; Indels
                                                         /note= "insulin family signature"
                    'note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                Goddard A,
Pitti RM,
                                                                                                                                                                                                                                                                                                                Ashkenazi AJ, Baker KP, Fong S, Hillan KJ, Mark MR, Marsters SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; Fig 6; 127pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||||| |:|| ||: | ||| || 26 vrlcgleyirtviyicassrw 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 VRLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                        15-MAR-2000; 2000WO-US06884.
                                                                                                                                                                                                                                  99US-0144758.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 66.7%
                                     121..136
125..131
                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                  2001-103149/11.
                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAF30052
                                                                                                      WO200105972-A1
Modified-site
                                                                                                                                                                                                                                  20-JUL-1999;
                                                                                                                                                25-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence
                                                                                                                                                                                                                                                                                                                                                             Wood WI;
                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
    δ
```

ô

```
RESULT 1
```

AAB53072 standard; Protein; 135 AA.

AAB53072;

28-FEB-2001 (first entry)

Human angiogenesis-associated protein PRO182, SEQ ID NO:41.

Human; anglogenesis-associated protein; PRO; endothelial cell growth, cardiac hypertropy; cardiavascular disorder; endothelial disorder; anglogenic disorder; atherosclerosis; osteoporosis; hypertension; myocardial infarction; diabetic retinopathy; rheumatoid arthritis; croins disease; psortasis; endometriosis; ulcer; wound healing; cancer; Alzheimer's disease; Huntington's disease; stroke; drug screening; gene therapy; transgenic animal.

Homo sapiens,

WO200053753-A2.

14-SEP-2000

2000WO-US00219 05-JAN-2000;

99US-0141037. 99US-0144758. 99US-0145698. 99WO-US20594. 99WO-US21090. 99WO-US21547. 99WO-US23089. 99US-0134287 99WO-US12252 99WO-US20111 99WO-US28409 99WO-US28564 99WO-US28565 01-SEP-1999; 08-SEP-1999; 15-SEP-1999; 20-JUL-1999; 15-SEP-1999; 08-MAR-1999 14-MAY-1999 02-JUN-1999 23-JUN-1999 05-0CT-1999; 30-NOV-1999 30-NOV-1999; 02-DEC-1999;

(GETH) GENENTECH INC.

Goddard A; MR. Marsters SA; Mark MR, Ma M, Wood WI; Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Ma Paoni NF, Pitti RM, Watanabe CK, Williams PM,

WPI; 2001-090793/10. N-PSDB; AAC97396 New isolated nucleic acid for producing a PRO polypeptide, analyzing genetic disorders and treating cardiovascular, endothelial or anglogenic disorders, such as atherosclerosis, wounds or cancer -

Claim 69; Fig 18; 293pp; English.

The invention relates to novel human angiogenesis-associated proteins designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding PRO proteins. The invention also relates to vectors and host cells comprising a PRO nucleic acid, the recombinant production of a PRO protein, PRO antibodies specific for a PRO protein, fusion proteins compounds which inhibit the expression of a PRO gene. The invention additionally encompasses methods of identifying modulators of PRO expression or activity; diagnosting a cardiovascular, endothelial or additionally encompasses methods of identifying modulators of PRO expression or activity diagnosting a cardiovascular, endothelial or mutations in a PRO gene, or the expression level of a PRO gene within a particular tissue; treating a cardiovascular, endothelial or angiogenic disorder via the administration of a PRO protein, PRO nucleic acid, or PRO agonist or antagonist; a retroviral gene therapy vector comprising a

Relaxin-like factor - useful as replacement for relaxin in treatment

(CONN-) CONNECTIVE THERAPEUTICS INC.

UNIV SOUTH CAROLINA

(UXSC-)

Schwabe C, Unemori E; WPI; 1997-051882/05.

96WO-US07399 95US-0484219.

16-MAY-1996; 07-JUN-1995;

.9-DEC-1996,

of, e.g. cardiovascular or neuro:degenerative disease

Claim 1; Page 48; 60pp; English

```
PRO nucleic acid; and methods of inhibiting or stimulating endothelial cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the administration of a PRO protein, or an agonist or antigonist thereof. PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO agonists and PRO antagonists may be used as therapeutic agents to treat cardiovascular, endothelial or angiogenic disorders, such as thereosclerosis, osteoporosis, myocardial infarction, hypertension, diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis, endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's disease, or stroke. PRO nucleic acids are additionally useful in the recombinant production of PRO proteins, as hybridisation probes to screen libraries to isolate cDNAs with sequence identity to PRO proteins, to analyse genetic disorders, and in gene therapy. PRO nucleic acids can also be used to produce transgenic animals useful for the development and screening of potential invention.
                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Forms disulphide bond with A chain Cysll"
22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ____/note= "Forms disulphide bond with A chain Cys24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A chain; B chain; relaxin-like factor; RLF; relaxin; cardiovascular disease; neurodegenerative disease; neurological disease; sinus bradycardia; depression; hair loss; collagen; scleroderma; fibronectin; insulin.
                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                          54.7%; Score 82; DB 22; Length 135; 66.7%; Pred. No. 0.00034; 1ve 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW07863 standard; peptide; 31 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                        26 vrlcgleyirtviyicassrw 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Relaxin-like factor B chain.
                                                                                                                                                                                                                                                                                                                                                                                                            7 VRLCGREFIRAVIFTCGGSRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                            Query Match 54.7
Best Local Similarity 66.7
Matches 14; Conservative
                                                                                                                                                                                                                                                                                               135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9640186-A1
                                                                                                                                                                                                                                                               invention.
                                                                                                                                                                                                                                                                                               Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW07863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW07863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                        QQ
     δ
```

```
The sequences given in AAW07862-63 represent the A and B chains of relaxin-like factor (RLF). RLF displaces bound relaxin tracer from the receptor to which it is bound. The RLF can be used to treat relaxin treatable conditions, esp. cardiovascular disease, neurodegenerative or neurological disease, sinus bradycardia, depression, hair loss or diseases related to uncontrolled or abnormal formation of collagen (e.g. scleroderma) or fibronectin. RLF can be radiolabelled for use in binding assays, and for relaxin receptor mapping. RLF shares primary and secondary homology to relaxin and insulin.
                                                                                                                                                                                                                                                                                                                                                          50.7%; Score 76; DB 18; Length 31; 55.0%; Pred. No. 0.00056; Live 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 55.09
Matches 11; Conservative
                                                                                                                                                                                                                                                                              31 AA;
                                                                                                                                                                                                                                                                                Sequence
        888888888888
```

ó

0; Gaps

Search completed: June 27, 2002, 16:08:09 Job time: 278 sec

:||| |:||:: ||| || 8 klcghhfvralvrvcggprw 27 8 RLCGREFIRAVIFTCGGSRW 27

QQ

οy

```
June 27, 2002, 16:08:44; Search time 28.78 Seconds (without alignments) 22:915 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                  231628
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                           US-09-781-077-2_COPY_26_52
150
1 RAAPYGVRLGGREFIRAVIFTGGGSRW 27
                                                                                                                                                                                                                                                                                                                                    231628 seqs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                             Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. /cgn2_6/ptodata/2/jaa/5A_COWB.pep:*
/cgn2_6/ptodata/2/jaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6A_COWB.pep:*
/cgn2_6/ptodata/2/jaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*

Issued_Patents_AA:*

Database :

	Description	Patent No. 5464756	Š	. 69 an	• • •	4	14,	9	7	5			No. 546475	ce 14.	-	10,		١.	Patent No. 5464756	Ge]		90	1, 4	1, Appl	Patent No. 5464756	NO 546475	No. 546475	ice 12, App	
SUMMARIES	ID	5464756-16	547	US-08-353-476-92	-950-720A-	US-08-484-219-4	õ	US-08-950-720A-6	-443-568	\sim	969	5464756-11	5464756-10	US-08-443-568B-14	PCT-US94-06997-14	US-08-443-568B-10	PCT-US94-06997-10	5464756-18	5464756-20	US-08-950-720A-12	-08-6	-08-353-476		158-706	6-1	5464756-9	9	US-08-443-568B-12	
	DB	9	9	7	٣	~	æ	m	-	7	2	9	9	П	Ŋ	Н	Ŋ	9	9	3	e	7	7	4	9	9	9	1	
	Ouery Match Length	30	29	40	135	31	101	135	29	53	29	32	33	52	. 52	77	77	162	164	185	185	33	59	29	35	32	32	150	
ф	Query Match	77.3	68.0	58.0	54.7	50.7	50.7	20.0	47.3	47.3	47.3	47.3	47.3	47.3	47.3	47.3	47.3	47.3	47.3	47.3	47.3	46.0	ď.	'n.	•	œ	36.7	5.	
	Score	116	102	87	83	97	92	75	71	71	71	71	71	71	71	71	71	7.1	71	71	71	69	9	68	29	57	55	53	
	Result No.	1	7	m	4	iO.	91	7	ထ	ָּ רַ	10	11	13	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	

Sequence 12, Appl Sequence 2, Appli Sequence 2, Appli Patent No. 5464756 Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Patent No. 532575 Sequence 1, Appli Patent No. 5489517 Patent No. 5489517 Patent No. 5489517 Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 5, Appli Sequence 5, Appli Sequence 17, Appli		.; o		; 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		Gaps		Gaps
Juency Ju		0;		0;
	L.;WILKINS, FOR THE	; Length 30; 0; Indels	D.; WILKINS, FOR THE	Length 29; ;; l; Indels
PCT - US94 - 06997 - 12 US-08 - 905 - 267 - 2 5464756 - 13 US-08 - 905 - 267 - 13 US-08 - 905 - 267 - 13 US-09 - 914 - 051 - 13 US-09 - 097 - 889 - 23 535.275 - 9 US-08 - 435 - 252 - 1 5480517 - 2 5480517 - 2 5480517 - 2 5480517 - 2 5480517 - 2 US-07 - 963 - 329A - 2 US-07 - 963	ALIGNMENTS J.; VANDLEN, RICHARD L.; WILKINS S AND COMPOSITIONS FOR THE 07/908,766 550	re 116; DB 6; d. No. 1.6e-10; Mismatches (N, RICHARE POSITIONS 6	re 102; DB 6; d. No. 1.7e-08 Mismatches
PPCT- US- US- US- US- SA- SA- SA- SA- SA- SA- SA- SA- SA- S	ALI J.;VANDE S AND CO '07/908,7	Score Pred. 3; Mis 27	.,VANDLE AND COM 7/908,76	Sco Pre 3;
	s J ESS S/0 92 7,5	.3%; .4%; e GSRW 	S J ESS 5/0 32 7,5.	* *
150 188 188 33 29 29 33 36 50 67 70 70 70 70	DENNIS LEL G. N: PROCE AXIN ON DATA: BER: US DATA: DATA: BER: 347.	77 86 ativ FTCG :	DENNIS LEL G. N: PROCE. AXIN AXIN AXIN DATA: BER: US, BER: US, DATA: DATA: AX7-198(68.0%; .larity 81.0%; .conservative
35.33 36.33 37.70 38.70	5464756 NAT: HENNER, DIANSURA, DANIEL DF INVENTION: 1 N HUMAN RELEAXI OF SEQUENCES: T APPLICATION I CATION NUMBER CATION NUMBER CATION NUMBER: CATION NUMBER: GATION NUMBER:	ch 1 Similarity 19; Conserv WRLGGREFIRAVI	4756 HENNER HENNER NVENTION NVENTION MAN REL SEQUENT TON NUM TON NUM ATE: 04	h Similarity 17; Conser
53 53 53 53 53 53 53 53 53 53 53 53 53 5	1 16 NO. NIC. NIC. NICE WITE NICE WITE	Query Match Best Local Si Matches 19; 6 GVRLC 1::	1. 2 APPLICANT: HENNER, DENNIS J. APPLICANT: HENNER, DENNIS J. TITLE OF INVENTION: PROCESS, OLATION HOWN RELAXIN UNDBER OF SEQUENCES: 42 UNGRENT APPLICATION DATA: APPLICATION NUMBER: US/07, PRIOR APPLICATION DATA: APPLICATION NUMBER: 347,557 FILING DATE: 01-JUL-1992 FILING DATE: 04-MAY-1989 IL DNO:15: LENGTH: 29	atc 3al
22 33 33 33 33 33 33 34 44 44 44 44 44 44	RESULT 5464756-; Patent; JAMES P 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Query Best Match Qy Db	RESULT 5464756 Patent AP AP 1 ISOLA TI CUI CUI PR 1 PR 1 SEQ ID 1	Query Ma Best Loc Matches

```
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Halluin, Albert P.
                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                           APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 435
                       Seattle
                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U
                                                                         98102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-950-720A-2
                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-484-219-4
                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                         GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Weininger, Arthur M
TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58.0%; Score 87; DB 2; I 70.0%; Pred. No. 3.6e-06; tive 3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st St., Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: CORKLIN, Darrell C.
APPLICANT: Lofton-Day, Catherine E.
APPLICANT: Lofk, Si
APPLICANT: Jaspers, Stephen R.
ITILE OF INVENTION: INSULIN HOMOLOG
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Bencen, Gerard H
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: GP-100
TELECOMMUNICATION INFORMATION:
TELEPRAN: (904) 375-8100
INFORMATION FOR SEQ ID NO: 92: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08950720A Patent No. 6046028
                                                                                                                                                         Sequence 92, Application US/08353476 Patent No. 5871902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZymoGenetics, Inc.
                       6 GVRLCGREFIRAVIFTCGGSR 26
                                           9 GIKLCGREFIRAIIFACGGSR 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 RLCGRDLIRAFIYLCGGTRW 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 RLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 40 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 58.0°
Best Local Similarity 70.0°
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 11 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                     CITY: Gainesville
STATE: Florida
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                               32606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE:
                                                                                                                   RESULT 3
US-08-353-476-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-353-476-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-950-720A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                         ŏ
                                                             q
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08484219;
Sequence 4, Application US/08484219;
Fatent No. 5911997
GENERAL INFORMATION:
FAPPLICANT: Schwabe, Christian
APPLICANT: Unemori, Elaine
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 82; DB 3; Length 155.
Pred. No. 6.5e-05;
Tred. Tredels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                      US/08/950,720A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/484,219
FILLING DATE: 07-JUN-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISCRATION NUMBER: 37,438
REFRENCE/CDCKET NUMBER: 96-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 VRLCGLEYIRTVIYICASSRW 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 VRLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54.78;
66.78;
                                            COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 54.77
Best Local Similarity 66.77
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein FRAGMENT TYPE: internal
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
```

```
Gaps
                                                                  ö
                  50.7%; Score 76; DB 3; Length 101;
55.0%; Pred. No. 0.00036;
Live 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.0%; Score 75; DB 3; 1
52.4%; Pred. No. 0.00068;
tive 5; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FestSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/950,720A
                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: CONKlin, Darrell C.
APPLICANT: Lofton-Day, Catherine E.
APPLICANT: Lofk, Si.
APPLICANT: Jaspers, Stephen R.
TILLE OF INVENTION: INSULIN HOMOLOG
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                         Sequence 6, Application US/08950720A Patent No. 6046028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 2, Application US/08443568B
; Patent No. 5759807
; GENERAL INFORMATION:
APPLICANT: Breece, Tim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37,438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 VRLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 VKLCGLDYVRTVIYICASSRW 46
                                                                                                   8 RLCGREFIRAVIFTCGGSRW 27
                                                                                                                       32 KLCGHHFVRALVRVCGGPRW 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Sawislak, Deborah A REGISTRATION NUMBER: 37,43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135 amino acids
                                         Best Local Similarity 55.09
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 206-442-667
TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-950-720A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98102
                                                                                                                                                                                                                    US-08-950-720A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-443-568B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                           Query Match 50.7%; Score 76; DB 2; Length 31; Best Local Similarity 55.0%; Pred. No. 0.00011; Matches 11; Conservative 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/950,720A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: CONKIIN, Darrell C.
APPLICANT: Lofton-Day, Catherine E.
APPLICANT: Lok, Si
APPLICANT: Jaspers, Stephen R.
TITLE OF INVENTION: INSULIN HOWOLOG
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
. 25,227
---- 7842-040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICALLO.
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
NAME: Sawislak, Deborah A
NAME: Sawislak, Deborah A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14, Application US/08950720A Patent No. 6046028 GENERAL INFORMATION:
      REGISTRATION NUMBER: 25.227
REFERENCE/DOCKET NUMBER: 7842
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854 3660
TELEFAX: 415-854 3694
TELEFAX: 6641 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RECISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 96.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                            8 RLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                S KLCGHHFVRALVRVCGGPRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: Single
TOPOLOGY: linear
MOLECULE TYPE: No. 6046028e
US-08-950-720A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 101 amino acids
                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-484-219-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-950-720A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                                                                                            δ
```

```
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RELAXIN-LIKE FACTOR AND METHODS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47.3%; Score 71; DB 1; Length 29; 57.1%; Pred. No. 0.00056; tive 3; Mismatches 6; Indels
                                       APPLICANT: Vandlen, Richard
APPLICANT: Daniel, Yansura
TITLE OF INVENTION: Process for Producing Relaxin
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/443,568B FILING DATE: 22-MAY-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                 ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: New York
COUNTRY: United States of America
ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7842-037
                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Schwabe, Christian
APPLICANT: Ormori, Elaine
TITLE OF INVENTION: RELAXIN-LIKE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08/080,354
Hayenga, Kirk
Rindersknecht, Ernst
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/080,35.
FILING DATE: 21-JUNE-1993
CLASSIFICATION: 435
ATTORNET: NEVERATION:
NAME: Abrams, Samuel B.
REGISTRATION NUMBER: 30,605
TELECOMMUNICATION INDERRATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/08484219
Patent No. 5911997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 IKLCGRELVRAQIAICGMSTW 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 VRLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 29 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 47.3°
Best Local Similarity 57.1°
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                            New York : U.S.A.
                                                                                                                                                                                           New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                      10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-443-568B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-484-219-5
                                                                                                                                                                                                                                  COUNTRY:
                        APPLICANT:
                                                                                                                                                                                                            STATE:
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 47.3%; Score 71; DB 2; Length 29; Best Local Similarity 57.1%; Pred. No. 0.00056; Matches 12; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10036
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06997
FILING DATE: 20-JUN-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: HAlluin, Albert P.
REGISTREMCE/DOCKET NUMBER: 7842-025-228
TELEPRENCE/DOCKET NUMBER: 7842-025-228
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-854-3660
TELEFAX: 415-854-3694
TELEFAX: 6614 PENNIS
TELECOMMUNICATION INFORMATION:
TELEFAX: 6614 PENNIS
SEQUENCE CHARACTERISTICS:
TURFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Genentech, Inc.
APPLICANT: Genentech, Inc.
APPLICANT: 460 Point San Bruno Boulevard
APPLICANT: South San Francisco, California
APPLICANT: United States of America
TITLE OF INVENTION: Process for Producing Relaxin
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                            7842-040
                                                                         US/08/484,219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application PC/TUS9406997 GENERAL INFORMATION:
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 7842
TELECOMMUNICATION INFORMATION: TELEPHONE: 415-84-3660
TELERAX: 415-84-364
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 29 amino acids
                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 IKLCGRELVRAQIAICGMSTW 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 VRLCGREFIRAVIFTCGGSRW 27
                                                            APPLICATION UMBER: US/OF FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-484-219-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: New York STATE: New York COUNTRY: U.S.A. ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
PCT-US94-06997-2
```

```
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
5464756-10
; PATENT NO. 5464756
; PATENT NO. 5464756
; JAMES A.; FANSURA. DANIEL G.
; JAMES A.; TANSURA. DANIEL G.
; ISOLATION HUMAN RELAXIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; PLING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 34,550
; FLING DATE: 04-MAY-1989
                                                                                                                                                                                                                                                  RESULT 11
5464756-11
;Patent No. 5464756
; APPLICANT: HENNER, DENNIS J.;VANDLEN, RICHARD L.;WILKINS,
                                                                       Query Match
47.3%; Score 71; DB 5; Length 29;
Best Local Similarity 57.1%; Pred. No. 0.00056;
Matches 12; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 47.3%; Score 71; DB 6; Length 32; Best Local Similarity 57.1%; Pred. No. 0.00062; Matches 12; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
47.3%; Score 71; DB 6; Length 33;
Best Local Similarity 57.1%; Pred. No. 0.00064;
Matches 12; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                JAMES A.; YANSURA, DANIEL G.

TITLE OF INVENTION: PROCESS AND COMPOSITIONS FOR THE

LISOLATION HUMAN RELAXIN
                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 42
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/908,766
FILING DATE: 01-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 347,550
FILING DATE: 04-MAY-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14, Application US/08443568B Patent No. 5759807
                                                                                                                                                     7 VRLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                        8 IKLCGRELVRAQIAICGMSTW 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 VRLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 IKLCGRELVRAQIAICGMSTW 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 VRLCGREFIRAVIFTCGGSRW 27

// MOLECULE TYPE: protein
PCT-US94-06997-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO:10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-08-443-568B-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO:11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5464756-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5464756-10
                                                                                                                                                       δ
                                                                                                                                                                                        QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 47.3%; Score 71; DB 1; Length 52; Best Local Similarity 57.1%; Pred. No. 0.001; Matches 12; Conservative 3; Mismatches 6; Indels
                                                              APPLICANT: Vandlen, Richard
APPLICANT: Vandlen, Richard
TILE OF INVENTION: Process for Producing Relaxin
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Genericch, Inc.
APPLICANT: Genericch, Inc.
APPLICANT: 460 Point San Bruno Boulevard
APPLICANT: South San Francisco, California
APPLICANT: United States of America
TITLE OF INVENTION: Process for Producing Relaxin
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                             E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/443,568B FILING DATE: 22-MAY-1995
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/080,354
FILING DATE: 21-JUNE-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7842-037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCT-US94-06997-14; Sequence 14, Application PC/TUS9406997; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
APPLICANT: Breece, Tim
APPLICANT: Hayenga, Kirk
APPLICANT: Rindersknecht, Ernst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Abrams, Samuel B. REGISTRATION NUMBER: 30,605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 78. TELECOMMUNICATION INFORMATION: TELEPHONE: 650-493-4935 TELEFAX: 650-493-5556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 VRLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 IKLCGRELVRAQIAICGMSTW 51
                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                       CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                      10036
                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-443-568B-14
                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
```

ô

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 47.3%; Score 71; DB 5; Length 52; Best Local Similarity 57.1%; Pred. No. 0.001; Matches 12; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Breece, Tim
APPLICANT: Hayenga, Kirk
APPLICANT: Rindersknecht, Ernst
APPLICANT: Vandlen, Richard
APPLICANT: Vandlen, Richard
APPLICANT: Daniel, Yansura
TITLE OF INVENTION: Process for Producing Relaxin
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,568B
FILING DATE: 22-MAY-1995
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 22,227
REFERENCE/DOCKET NUMBER: 7842-025-228
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1155 Avenue of the Americas CITY: New York COUNTRY: U.S.A. ZIP: 10036
                                                                                     APPLICATION NUMBER: PCT/US94/06997 FILING DATE: 20-JUN-1994 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/08443568B Patent No. 5759807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/080,354
FILING DATE: 21-JUNE-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Abrams, Samuel B.
REGISTRATION UNDRER: 30,605
REFERENCE/DOCKET NUMBER: 7842
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-555
TELERA: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 VRLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31 IKLCGRELVRAQIAICGMSTW 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein pcr-us94-06997-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
US-08-443-568B-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
```

,				
				,
			·	•

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on:

June 27, 2002, 16:09:27; Search time 36.01 Seconds (without alignments) 72.047 Million cell updates/sec

1 RAAPYGVRLCGREFIRAVIFTCGGSRW 27 US-09-781-077-2_COPY_26_52 Perfect score: Sequence: Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTE

	¥ .	Description		י משחקי	,	ins	Levdia insulin-lik	_	1 1	Н	-	100		,	D		1	pr			relaxin precursor		hypothetical prote	relaxin - horse (f	relaxin B,C and A	hypothetical prote	relaxin precursor	Suppressor of hair	relaxin - baboon (transcription fact
SUMMARIES		ID	A26463	RXRKOT	A29543	B53024	A53024	S42786	S42784	S42783	A44559	A60982	S42778	B32201	S48082	A53879	I56451	A34936	A58793	A32201	RXPG	S42781	T27987	A49739	I47053	T29014	RXRT	A48586	S42785	T10897	S71427
		Length DB	54 2	4					57 2				57 2						31 2					48	m	a		w		œ	
ď	Ollery	'	77.3	64.0	58.0	50.7	50.0	48.0	47.3	47.3	47.3	47.3	42.0	40.7	40.7	40.0	38.0	38.0	37.3	36.7	36.7	36.0	35.3	34.7	34.7	34.0	34.0	34.0	33.3	33.3	
		Score	116	96	87	92	75	72	71	71	71	71	63	61	61	9	57	57	26	55	25	54	53	52	52	51	51	51	20	20	20
	Result	NO.	Н	73	e	4	ഹ	9	7	ω,	0	10	11	12	13	14	15	16	17	18	19	20	77	22	573	74	25	56	27	28	29

C:Species: Odontaspis taurus (sand tiger)
C:Species: O-Sep-1981 #sequence_revision 26-May-1995 #text_change 31-Mar-2000
C:Accession: A01616
R:Gowan, L.K.; Reinig, J.W.; Schwabe, C.; Bedarkar, S.; Blundell, T.L.
FEBSI Lett. 129, 80-82, 1981
A:Title: On the primary and tertiary structure of relaxin from the sand tiger shark A:Reference number: A01616; MUID:82004703
A:Reference number: A01616
A:Rolecule type: protein
A:Reference i;2-19;21-44 <GGW>
R:Reliesbach, E.E.; Gowan, L.K.; Schwabe, C.; Steinetz, B.G.; O'Byrne, E.; Callard, Eur. J. Blochem. 161, 335-341, 1986

> 6 GVRLCGREFIRAVIFTCGGSRW 27

> > RESULT RXRKOT

δλ Q

2inc finger 5 prot 127989 T27989 T4466 T4466 T54734 T5734 TNEN TNEN TNEN TNII	RESULT 1 A26463 C:Dete: 19. Nov-1988 #sequence_revision 26-May-1995 C:Date: 19.Nov-1988 #sequence_revision 26-May-1995 Eur. J. Biochem. 161, 335-341, 1986 A:Title: 1solation, purification, and the sequence of relaxin from spiny dogfish (;A. Notestence number: A91179; MUD:87054035 A:Reference number: A91179; MUD:87054035 A:Reference protein A:Residues: 'E', 2-30 <	1-30/Domain: chain B #status experimental ACHB> 31-54/Domain: chain A #status experimental ACHB> 1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental 13-41,25-54,40-45/Disulfide bonds: #status predicted Query Match 77.3%; Score 116; DB 2; Length 54; Best Local Similarity 86.4%; Pred. No. 2.4e-10; Matches 19; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
2 5416/ 2 72796/ 2 74744/ 2 7473/ 1 INEN 1 INEN 2 7511/ 2 7511/ 2 7611/ 2 761/	ments) (spiny control	experion carbox conds:
449 106 106 107 107 107 107 107 107 107 108 108 108 108 108 108 108 108 108 108	RESULT A26463 C.Selaxin - spiny dogfish (fragments) C.Species: Squalus acanthias (spiny dogfis) C.Date: 19-Nov-1988 #sequence_revision 26 C.Accession: B26463; A26463 R.Bullesbach, E.F.; Gowan, L.K.; Schwabe, Aritle: Isolation, purification, and the Aritle: Protein A.Recession: B26463 A.Accession: B26463 A.Rectimental source: ovary A.Molecule type: protein	nain B #status en hain A #status en pyrrolidone con 45/Disulfide bor 77.3%; Conservative
.0000	dogfis lus aca 1188 #s 1988 #s 6463; 6463; 101, pu hor, pu hor, pu cer 6463 1. 2 prote 7. 2 prote 8. 5 prote 8. 5 prote 1. 6463 1. prote 8. 5 prote 1. prot	chain B n. chain A site: pyrr ,40-45/Dis
444 44 00000000000000000000000000000000	RESULT 1 A26463 relaxin - spiny dogfish (fragorisheris Squalus acanthias C; Species: Squalus acanthias C; Date: 19-Nov-1988 #sequence C; Accession: B26463 A26463 R: Bullesbach, E.E.; Gowan, L. Eur J. Biochem. 161, 335-341 A; Title: Isolation, purificat A; Reference number: A91179; MA; Reference number: A91179; MA; Residues: 'E', 2-30 cotain A; Residues: 'A, Accession: A6463 A; Residues: 'A, A, Bxperimental source: ovary A; Note: the amino-terminal re A; Rocession: A6463 A; Residues: 'A, Syperimental source: ovary C; Superfamily: insulin C; Reyorduct: relaxin C; Reyorduct: relaxin A, A-54 Product: relaxin A creaming: pyroglut	1-30/Domain: 031-54/Domain: 1/Modified sit 13-41,25-54,46 Query Match Best Local Sir Matches 19;
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT A26463 Telaxin C; Spate: C; Date: C; Caccess R; Bulles A; Refiele A; Residu A;	F;1-30/DO F;31-54/D F;1/Modif F;13-41,2 Query M Best Lo Matches

```
A; Cross-references: GDB:230307; OMIM:146738
                                  A; Map position: 19p13.2-19p12
A; Introns: 64/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                                                                                                                           a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leydig insulin-like protein precursor - human (5/5pecies: Homo sapiens (man) (2/5pecies: Homo sapiens (man) (2/5pecies: Homo sapiens (man) (2/5pecies: Homo 1994 #sequence_revision 03-May-1994 #sequence_revision 03-May-1994 #sequence_revision 03-May-1994 #sequence_revision 03-May-1994 #sequence_revision 03-May-1994 #sequence number: Adham, I.M.; Brosig, B.; Gastmann, A.; Mattei, M.G.; Engel, W. A;Title: Structural organization of the porcine and human genes coding for a Leydig cell A;Reference number: A53024; MUID:94292172
A;Title: Isolation, purification, and the sequence of relaxin from spiny dogfish (Squalu A;Reference number: A91179; MUID:87054035
A;Contents: annotation; sequence revision
A;Note: the carboxyl-terminal sequence of chain B was determined to be Arg-Trp
C;Superfamily: insulin
C;Keywords: pyroglutamic acid
F;1.19/Domain: chain B (fragments) #status experimental <CHB>
F;21-44/Domain: chain B (fragments) #status experimental <CHB>
F;1.4/Domain: chain B (fragments) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Raja erinacca (little skate)
C;Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 16-Feb-1997
C;Accession: A29543; Schwabe, C.; Callard, I.P.
Biochem. Biophys. Res. Commun. 143, 273-280, 1987
A;Tille: Relaxin from an oviparous species, the skate (Raja erinacea).
A;Reference number: A29543; MUID:87156758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-131 <BUR>
A; Cross-references: GB:X73637
R; Burkhardt, E.; Adham, I.; M; Hobohm, U.; Murphy, D.; Sander, C.; Engel, W.
Hum. Genet. 94, 91-94, 1994
A; Title: A human cDNA coding for the Leydig insulin-like peptide (Ley I-L).
A; Reference number: 154278; MUID:94307715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:S72482; NID:g632798; PIDN:AAB31371.1; PID:g632799 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: B53024
A;Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58.0%; Score 87; DB 2; Length 64; 70.0%; Pred. No. 5.9e-06; Live 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          64.0%; Score 96; DB 1; Length 44; 80.0%; Pred. No. 1.9e-07; 2: Indels Live 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: 154278
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  relaxin - little skate (fragments)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 RLCGRDLIRAFIYLCGGTRW 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QLCGRGFIRAIIFACGGSRW 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 RLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 RLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 70.09
Watches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: ovary C; Superfamily: insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein A; Residues: 1-64 <BUL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-131 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: GDB: INSL3
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A29543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
```

```
A.Accession: A53024
A.Status: preliminary; not compared with conceptual translation
A.Rocession: A53024
A.Status: preliminary; not compared with conceptual translation
A.Molecule type: DNA
A.Molecule type: DNA
A.Forsion: 1-131 < GBTS
A.Forsion: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leydig insulin-like protein precursor - pig
N;Alternate names: Ley I-L
C;Species: Sus scrofd domestic pig)
C;Species: Sus scrofd domestic pig)
C;Date: 03-May-1994 #text_change 05-Nov-1999
C;Accession: A53024; A49687
C;Accession: A53024; A49687
B;Burkhardt, E; Adhan, I.M.; Brosig, B.; Gastmann, A.; Mattei, M.G.; Engel, W.
A;Title: Structural organization of the porcine and human genes coding for a Leydig of A; Reference number: A53024; MUID:94292172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F)1-24/Domain: signal sequence #status predicted <SIG>F;25-56/Domain: Leydig insulin-like protein chain # #status predicted <BCH>F;55-105/Domain: connecting C peptide #status predicted <CPEP>F;57-105/Domain: connecting C peptide #status predicted <CRP>F;106-131/Domain: Leydig insulin-like protein chain A #status predicted <ACH>F;106-131/Domain: Leydig insulin-like protein chain A #status predicted <ACH>F;106-131/Domains Company Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Pan troglodytes (chimpanzee)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-166 <EVA>
A;Cross-references: EMBL:227245; NID:g416109; PIDN:CAA81758.1; PID:g416110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: testis
A; Note: sequence extracted from NCBI backbone (NCBIN:140859, NCBIP:140860)
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.0%; Score 75; DB 2; Length 131; 55.0%; Pred. No. 0.0007; tive 4; Mismatches 5; Indels
50.7%; Score 76; DB 2; Length 131;
55.0%; Pred. No. 0.0005;
iive 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, November 1993
A;Reference number: $42776
A;Accession: $42786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     relaxin 2 precursor - chimpanzee (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 RLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 KLCGHHFVRALVRLCGGPRW 51
                                                                                                                                                                                                                                                                                                                                                        8 RLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 KLCGHHFVRALVRVCGGPRW 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 55.0%
Matches 11; Conservative
                                  Query Match 50.79
Best Local Similarity 55.09
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: GB: X58369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Map position: 19p13.2-p12
A;Introns: 64/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-131 <ADH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: S42786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: A49687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: INSL3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
```

Gaps

; 0

6; Indels

Pred. No. 0.0035; 3; Mismatches (

57.1%;

Best Local Similarity 57.1 Matches 12; Conservative

27

7 VRLCGREFIRAVIFTCGGSRW

δŽ

N; Alternate names: preprorelaxin 1

relaxin 1 precursor - human

C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 07-Oct-1994 #text_change 18-Jun-1999
C;Accession: B05092; A44559
R;Hudson, P.; John, M.; Crawford, R.; Haralambidis, J.; Scanlon, D.; Gorman, J.; Treg

A; Accession: B05092

```
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          542783
relaxin 1 precursor - chimpanzee (fragment)
c;Species: Pan troglodytes (chimpanzee)
c;Species: Pan troglodytes (chimpanzee)
c;Accession: S42783
R;Evans, B.B.
submitted to the EMBL Data Library, November 1993
A;Reference number: S42776
A;Reference number: S42776
                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:227225; NID:g415996; PIDN:CAA81739.1; PID:g415997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C'Superfamily: insulin
C:Keywords: disulfide bond; hormone
F;1-33/Domain: relaxin chain 2B (fragment) #status predicted <RXB2>
F;34-57/Domain: relaxin chain 2A (fragment) #status predicted <RXA2>
                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                           Fil-5/Domain: signal sequence (fragment) #status predicted <SIG>Fi6-166/Product: relaxin 2 #status predicted <MAT>
                                                                                                  Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.3%; Score 71; DB 2; Lengtn 57,7 1%; Pred. No. 0.0013; 6; Indels
                                                                                                                               6; Indels
                                                                                           48.0%; Score 72; DB 2; 57.1%; Pred. No. 0.0024;
                                                                                                                          3; Mismatches
                                                                                                                                                     7 VRLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                        8 IKLCGRELVRAQIAICGMSTW 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 VRLCGREFIRAVIFTCGGSRW 27
                                                                                        Query Match
Best Local Similarity 57.1'
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 57.1
Matches 12; Conservative
                                                                                                                                                                                                                                                                 relaxin - gorilla (fragments)
A;Gene: rlx2
C;Superfamily: insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-166 < EVA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                     οχ
                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
```

```
A)Cross-references: GB.X00949; NID:g35932; PIDN:CAA25461.1; PID:g35933
R;Hudson, P.; Haley, J.; John, M.; Cronk, M.; Crawford, R.; Haralambidis, J.; Tregear Nature 301, 628-631, 1983
A;Title: Structure of a genomic clone encoding biologically active human relaxin.
A;Reference number: A44559; MUID:83141755
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-185 <HU2>
A;Cross-references: GB:X00949; NID:g35932; PIDN:CAA25461.1; PID:g35933
C;Comment: Relaxin is an ovarian hormone that acts with estrogen to produce dilation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 08-Dec-2000
C;Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 08-Dec-2000
C;Accession: A05092; A60982
R;Hudson, P.; John, M.; Crawford, R.; Haralambidis, J.; Scanlon, D.; Gorman, J.; Treg EMBO J. 3, 2333-2339, 1984
A;Title: Relaxin gene expression in human ovaries and the predicted structure of a human ovaries. A;Reference number: A05092; MUID:85051298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:X00948; NID:g35926; PIDN:CAA25460.1; PID:g35927
R;Stults, J.T.; Bourell, J.H.; Canova-Davis, E.; Ling, V.T.; Laramee, G.R.; Winslow,
Biomed. Environ. Mass Spectrom. 19, 655-664, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.Map position: 9pter-9q12
C.Superfamily: insulin
C.Superfamily: insulin
C.Superfamily: insulin
C.Superfamily: insulin
C.Superfamily: insulin
C.Superfamily: signal sequence #status predicted <BGS
F.1-25/Domain: relaxin 1 chain B #status predicted <MAT>
F.50-57,162-185/Product: relaxin 1 #status predicted <AMT>
F.58-158/Domain: relaxin 1 connecting C peptide #status predicted <CPEP>
F.162-185/Domain: relaxin 1 chain A #status predicted <ACH>
F.351-172,47-185,171-176/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 47.3%; Score 71; DB 1; Length 185; Best Local Similarity 57.1%; Pred. No. 0.0038; Matches 12; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: GDB:119552; OMIM:179730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       relaxin 2 precursor [validated] - human N;Alternate names: preprorelaxin 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 VRLCGREFIRAVIFTCGGSRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32 IKLCGRELVRAOIAICGMSTW
A; Molecule type: DNA
A; Residues: 1-185 <HU1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-185 < HUD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: A05092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disulfide bonds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Genetics:
A; Gene: GDB: RLN1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
```

C;Keywords: disulfide bond; hormone C;Keywords: disulfide bond; hormone F;1-5/Domain: signal sequence (fragment) #status predicted <SIG> F;6-166/Product: relaxin 1 #status predicted <MAT>

C; Superfamily: insulin

A; Gene: rlx1

Length 166;

DB 2;

47.3%; Score 71;

```
A; Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              848082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  엄
                                                                                                                                                                                                                                                                                                                             A/cole: Obs.Nun.
A/cole: Obs.Nun.
A/cross-references: GDB:119553; OMIM:179740
A/Map position: 9pter-9q12
A/Map position: 9pter-9q12
C/superfamily: insulin
C/sup
A;Title: Structural characterization by mass spectrometry of native and recombinant humd
A;Reference number: A60982; MUID:91167739
A;Accession: A60982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 relaxin - minke whale (fragments)
C;Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
C;Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
C;Species: 13-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 18-Jun-1993
C;Accession: B32201
R;Schwabe, C.; Buellesbach, E.E.; Heyn, H.; Yoshioka, M.
J. Biol. _Chem. 264, 940-943, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            relaxin - gorilla (fragments)
C;Species: Gorilla gorilla (gorilla)
C;Date: 06-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C;Accession: S42778; S42777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: S42777
A;Molecule type: DNA
A;Rolecule type: DNA
A;Residues: 34-57 <EVX>
A;Cross-references: EMBL: Z27226; NID:g415948; PIDN:CAA81740.1; PID:g415949
A;Note: chain 1A
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-33 <EVA>
A; Cross-references: EMBL:227227; NID:9415950; PIDN:CAA81741.1; PID:9415951
A; Note: chain 1B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C, Superfamily: insulin
C; Keywords: disulfide bond; hormone
F;1-33/Domain: relaxin chain lB (fragment) #status predicted <RXB1>
F;34-57/Domain: relaxin chain lA (fragment) #status predicted <RXA1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47.3%; Score 71; DB 1; Length 185; 57.1%; Pred. No. 0.0038; tive 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 42.0%; Score 63; DB 2; Length 57; Best Local Similarity 52.4%; Pred. No. 0.021; Matches 11; Conservative 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, November 1993
A;Reference number: $42776
A;Accession: $42778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 VRLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 IKLCGCELVRAQIAICGMSTW 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 VRLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 IKLCGRELVRAOIAICGMSTW 52
                                                                                                                                                    A; Molecule type: protein
A; Residues: 25-53;162-185 <STU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 57.1%
                                                                                                                                                                                                                                                                                                    A; Gene: GDB: RLN2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: rlx1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
S42778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B32201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
```

```
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-185 <EVAA
A;Residues: 1-185 <EVAA
A;Coross-references: EMBL:227088; NID:9414780; PIDN:CAA81611.1; PID:9414781
B;Buellesbach, E.E.; Schwabe, C.
Biochem. Biophys. Res. Commun. 196, 311-319, 1993
A;Title: Mouse relaxin: synthesis and biological activity of the first relaxin with a A;Reference number: PN0626; MUID:94030011
A;Accession: PC2067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 161-185 <BU2>
A; Note: proteins with and without 184-Tyr were synthesized, their biological activiti C; Superfamily: Insulin C; Reywords: hormone F; 23-57,161-185/Product: relaxin #status experimental <MAT> F; 23-57/Domain: chain B #status experimental <CHB> F; 161-185/Domain: chain A #status experimental 
A;Title: Cetacean relaxin. Isolation and sequence of relaxins from Balaenoptera acuto A;Reference number: A32201; MUID:89093167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 16-Jul-1999
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 16-Jul-1999
C;Accession: S48082; PC2067; PN0626
R;Evans, B.A.; John, M.; Fowler, K.J.; Summers, R.J.; Cronk, M.; Shine, J.; Tregear, J. Mol. Endocrinol. 10, 15-23, 1993
A;Title: The mouse relaxin gene: nucleotide sequence and expression.
A;Reference number: S48082; MUID:93199663
A;Accession: S48082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  relaxin - dog (fragments)
C;Species: Canis lupus familiaris (dog)
C;Species: Canis lupus familiaris (dog)
C;Species: 27-Sep-1994 #sequence_revision 26-May-1995 #text_change 26-May-1995
C;Accession: B58879; A53879
R;Stewart, D.R.; Henzel, W.J.; Vandlen, R.
J; Protein Chem. 11, 247-253, 1992
J; Protein Chem. 11, 247-253, 1992
A;Title: Purification and sequence determination of canine relaxin.
A;Reference number: A53879; MUID:93000391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40.7%; Score 61; DB 2; Length 185; 52.6%; Pred. No. 0.12; tive 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                  Length 54;
                                                                                                                                                                                                                                                                                                                                                                   8; Indels
                                                                                                                                                                                                                                                                                                  40.7%; Score 61; DB 2; 42.9%; Pred. No. 0.039;
                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                   4,
                                                                                                                                                                                                                                                                                                                                                                                                                                       7 VRLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 IKACGRELVRLWVEICGSVRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 VRLCGREFIRAVIFICGGS 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 IRMCGREYARELIKICGAS 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 52.67
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     relaxin precursor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein A; Residues: 23-57 <BUE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
A; Residues: 161-185 <BU2>
                                                                                                             A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-54 <SCH>
C;Superfamily: insulin
                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: PN0626
                                                                           A; Accession: B32201
                                                                                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13
                                                                                                                                                                                                                                                                                                                                                                             Matches
```

S

```
A Preparimental source: placenta
A Notes: Sequence extracted from NCBI backbone (NCBIP:115401)
A Accession: A53879
A Accession: A53879
A Accession: A53879
A Accession: A53879
A Maccession: A53879
A
```

Search completed: June 27, 2002, 16:09:27 Job time: 211 sec

:: |||| :|| | || | 8 IKACGRELVRAQIAICGKS 26

g

	· •	
•		
		•
		*

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

June 27, 2002, 16:16:51; Search time 18.68 Seconds (without alignments) 55.965 Million cell updates/sec Run on:

US-09-781-077-2_COPY_26_52 150

Title: Perfect score: Sequence:

1 RAAPYGVRLCGREFIRAVIFTCGGSRW 27

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

. . . .

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description			caspis	ra]a	DOMO!	P51460 homo sapien	s sns	pos	mus	P51455 pan troglod	pan 1	homo	homod	rattu	-		P11184 balaenopter	P47932 mus musculu	_	P11185 balaenopter		P01348 sus scrofa	Q9trm8 canis famil	Q9qy05 mus musculu	Q09627 caenorhabdi	Q9wv41 rattus norv	P22969 equus cabal	4 caeno	P01347 rattus norv	5 drosop	0	Parameter 9	, and	0.00
	ID	RELX SOHAC	1 ~	DELY DATED	TMI C HIMAN	THE THE PERSON	INL3_HUMAN	INT3_PIG	INL3_BOVIN	INL5_MOUSE	REL2_PANTR	REL1_PANTR	REL1_HUMAN	REL2_HUMAN	INL3_RAT	INL3_CALJA	INL3_MOUSE	RELX_BALAC		RELX_MACMU	RELX_BALED	RELX_MESAU	RELX_PIG	RELX_CANFA	INT6_MOUSE	ILB2_CAEEL	INL6_RAT	RELX_HORSE	ILB5_CAEEL	RELX_RAT	SUHW_DROAN	ZFG1_CHICK	ZFG1_HUMAN	ZFG1_MOUSE	ILB1_CAEEL
	DB	: -	-	- ۱	-	٠,	٠,	٦.	-	Н	-	Н.	-	Н,	Н	-	Η.	Н	7	7	~	Н.	-	Н.	н,	-	-	Т	Н,	-	٦	Н	Н	۲	
	engt	54	44	64	125	າເ	n	7	n	m	166	9	ω,	8	\circ	m	122	54	185	185	54	177	182	177	191	907	188	182	112	186	886	448	449	449	106
æ	Query	77.3	64.0	~	>	• c	٠	· •	·.	· ·		٠,	٠,	47.3	٠,	٠.	4.	40.7	· .		36.7	36.7	٠,	o 1	36.0	O I	Ω,			-	-	m	m	m	m
		116	96	87	. 6	7.0	7 0	0,1	2 !	75	7.5	, T	17	17	0/	60	9,0	ΙĢ	Į.	27	Ω t	ς, L	ა ა	54	7.04	0.0	501	75	51	I S	21	20	20	20	49.5
	Result No.		7	m	4	י ער) (d	9 6	~ (x 0 0	ט פ	10		12	1.5	T .	T?	0 r	77	87 F	61	0 7	77	77	57	4 6	7.0	9 1	700	87	67	30	31	32	33

RESULT 2 RELX_ODOTA

us nch bdi ien sa rce rce ulu amu on nov s m			°°
hydrolagus callorhynch caenorhabdi homo sapien dasyatis sa cavia porce mus musculu hippopotamu petromyzon dasypus nov didelphis m	Chondrichthyes; lus.	ny IS NOT TWO	Gaps
236 1 2 2 2 3 6 1 2 2 3 6 1 3	icht	yrn Spi ES BY	6
P09536 P131809 P09536 Q095281 P81191 P81191 P61333 Q05227 Q03554 P61309 P92669	ondr s.	from sp from sp SPECIES SPECIES	ID. 54;
	rci	etz B.G., O'B elaxin from PAROUS SPECI CHAIN LINKED	LIC ACID C64; Length 5. Indels
	rata ; Sq	einetz B.G oof relaxin oviparous N a CHAIN ;	XYLIC CRC64 Len ,
	SQUAC STANDARD; PRT; 54 AA. PELLX.SQUAC STANDARD; PRT; 54 AA. PELLX.SQUAC STANDARD; PRT; 54 AA. 01-0CT-1989 (Rel. 12, Created) 10-TEB-1994 (Rel. 28, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) Relaxin. Squalus acanthias (Spiny dogfish). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Elasmobranchii; Squalea; Squaloidei; Squalidae; SqualosarxISSUE=Ovary; SEQUENCE. TISSUE=Ovary. TISSUE=Ovary. TISSUE=Ovary. TISSUE=Ovary. TISSUE=Ovary.	of of NN A	
SNTS	54 A odate upda 1, Ve	C., S uence IN A AND AND Xin.	CHAIN CHAIN NE CAR! N. N. AD32A5; AD32A5; ches
INS_HYDCO INS_CALMI ILB3_CAELL ILB3_CAELL INLG_HUMAN RELX_DASSA RELX_CAVPO ZF39_MOUSE NUSM_HIPAM NUSM_DETMA NUSM_DASNO NUSM_DIDMA NUSM_DASNO NUSM_MACRO	ce up	the sequence 1986). RELAXIN IN AN B CHAIN AND Feted. INSULIN/IGF,	RELAXIN B CHAIN. RELAXIN A CHAIN. PYRROLIDONE CARB INTERCHAIN. INTERCHAIN. 1B7206773AD32A5B Score 116; DB 1 Pred. No. 6.38-13. 3; Mismatches 27
INS_C INS_C ILB3_C INL6_I INC6_I NU5M_I NU5M_I NU5M_I NU5M_I	PRT; Juenc Jotat Lsh). Cran	Schwabe the sec 1986). RELAXIN B CHAIN ELEGINATION ELEGINATI	RELAXIN RELAXIN PYRROLII INTERCH INTERCH IB72067 ISCOF 1: Pred. N
	E section of the sect	Sec 7	ייש אי שי
	D; Crest Last Last ny ords	L.K. hias, safe as a second control of the s	200 201 211 211 211 210 MW 210
859 107 107 107 100 100 100 100 100 100 100	STANDARD; 1. 12, Cr 1. 28, La 1. 40, La as (Spiny zoa; Chor squalea;	E., Gowan L.K. urification, a tlus acanthias) tem. 161:335-34. THE FUNCTION THE F	11
rrr00000000	STA eel. eel. ias azoa 7; Sqf	rifical description of the last action of the last	11 11 11 11 11 11 11 11 11 11 11 11 11
	9 (R 11 (R 11 (R 11 (R 11 (R 11 (R 11 (R 11 (R)))	E.E. Janali Ja Janali Janali Janali Janali Janali Janali Janali Janali Janali J	33 33 31 11 22 4 4 6 54 7 6 6 6 7 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	L.SQUAC STANDARD; PEDA. SQUAC STANDARD; PLOTS. SQUAC STANDARD; Ol-OCT-1989 (Rel. 12, Cr. Ol-CCT-2001 (Rel. 28, La 16-OCT-2001 (Rel. 40, La Relaxin. Squalus acanthias (Spiny Eukaryota; Metazoa; Chor Elasmobranchii; Squalea; (I) TISSUENCE.	Bullesbach E.E., Gowan L.K. Callard I.P.; "Isolation, purification, dogiish (Squalus acanthias, Eur. J. Biochem. 161:335-3	in family; Hormone. 7
	SQUAC RELX_SQU P11953; 01-0CT-1 01-FEB-1 16-0CT-2 SQUALUS EUKATYOL ELASMODE NCBL_TAX (1)	llesh llarc solat solat fish fish vET vET vET vET vET vET vET vET vET vET	
88888888888888888888888888888888888888	RESULT 1 RELX_SQUAC 11D RELX_SQUAC 11D RELX_SQUAC 01-0CT DT 01-0CT DT 01-0CT DE Relaxi 0C ELBAXI	Bull Call Call Call Call Call Call Call C	Insulin family; Hormo CHAIN 1 3 3 3 3 3 3 3 3 3
	REESI TO TO TO DI DI DI DI DI DI OC OC OC OC OC OC OC OC OC OC OC OC OC		KW FT FT FT FT SO OU Be Ma

N

```
DISULFID
                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                            INL5_HUMAN
                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                            Odontaspis taurus (Sand tiger shark) (Eugomphodus taurus).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Chondrichthyes:
Elasmobranchii; Galeomorphii; Galeoidea; Lamniformes; Odontaspididae;
                                                                                                                                          Gowan L.K., Reinig J.W., Schwabe C., Bedarkar S., Blundell T.L.; "On the primary and territy structure of relaxin from the sand tiger shark (odontaspis taurus)."; FEBS Lett. 129:80-82(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Raja erinacea (Little skate).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Chondrichthyes;
Blasmobranchii, Squalea, Hypnosqualea, Pristiorajea, Batoidea,
Rajiformes, Rajidae, Raja.
NCBI_TaxID=7782;
                                                                                                                                                                                                           MEDLINE-87054035; PubMed-3780747;
Bullesbach E.E., Gowan L.K., Schwabe C., Steinetz B.G., O'Byrne E.,
                                                                                                                                                                                                                                        "Isolation, purification, and the sequence of relaxin from spiny dogfish (Squalus acanthias).";
Eur. J. Biochem. 161:335-341(1986).
-i- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .,0
                                                                                                                                                                                                                                                                                          -1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64.0%; Score 96; DB 1; Length 44;
80.0%; Pred. No. 5.2e-08;
tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                               INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              6122F6604C660607 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-07T-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                   21-JUL-1986 (Rel. 01, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                        RELAXIN B CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                           RELAXIN A CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 AA.
  44 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY
                                                                                                                                                                                                                                                                                                                         InterProj IPR000739; Insulin_IGF_relaxin.
Paran, PR00049; Insulin, 1.
SMART; SW00078; IIGF, 1.
PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Ovary;
MEDLINE=87156758; PubMed=3827922;
                                                                                                                                     MEDLINE-82004703; PubMed-7274472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QLCGRGFIRAIIFACGGSRW 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 RLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                              4730 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 80.03
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                    Insulin family; Hormone.
  STANDARD;
                                                                                                                                                                                                                                                                                                                 PIR; A01616; RXRKOT.
                                                                                                                                                                                                                                                                                   DISULFIDE BONDS.
                                                     Relaxin (Fragments).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 AA;
                                                                                                       NCBI_TaxID=30501;
                                                                                                                                                                                                   REVISION TO 20.
                                                                                                                                                                                                                               Callard I.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RELX_RAJER
  RELX_ODOTA
                                                                                               Carcharias
                                                                                                                                                                                                                                                                                                                                                                                                  NON_CONS
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                               NON_CONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                             SEOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                       MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RELX_RAJER
  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -:-SUBUNIT: HERRODIAN OF A B CHAIN AND AN A CHAIN LINKED BY TWO DISULRIDE BONDS (BY SIMILARITY).
-:-TISSUE SPECIFICITY: HIGHLY EXPRESSED IN RECTUM WITH LOWER LEVELS IN UTERUS AND ASCENDING AND DESCENDING COLON.
-:-SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lok S., Jaspers S.; "Indentification of INSL5, a new member of the insulin superfamily."; "Indentification of INSL5, a new member of the insulin superfamily."; Genomics 60:50-56(1999).

-:- FUNCTION: MAY HAVE A ROLE IN GUT CONTRACTILITY OR IN THYMIC DEVELOPMENT AND REGULATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-99389725; PubMed=10458910;
Conklin D., Lofton-Day C.E., Haldeman B.A., Ching A., Whitmore T.E.,
Bullesbach E.E., Schwabe C., Callard I.P.;
"Relaxin from an oviparous species, the skate (Raja erinacea).";
Biochem. Biophys. Res. Commun. 143:273-280(1987).
-:- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Insulin-like peptide INSLS precursor (Insulin-like peptide 5).
                                                                                                                                                   -i- SUBCELLULAR LOCATION: Secreted.
-i- SUBCELLULAR LOCATION: Secreted.
-i- SUBLIARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
PIR; A29543; A29543.
HSSP; P04090; 6RLX.
Interpro; IPR000739; Insulin_IGF_relaxin.
FFAM: SM00078; Insulin; 1.
SMART; SM00078; ILGF; 1.
PROSITE: FS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58.0%; Score 87; DB 1; Length 64; 70.0%; Pred. No. 1.7e-06; Live 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E7AC62B8BA81F49D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RELAXIN A CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RELAXIN B CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000739; Insulin_IGF_relaxin.
SMART; SM00078; IIGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERCHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERCHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF133816; AAD29686.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 RLCGRDLIRAFIYLCGGTRW 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 RLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7499 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 58.0
Best Local Similarity 70.0
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Insulin family; Hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                      DISULFIDE BONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIM; 606413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INL5_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_CONS
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                    INLIALHUMAN STANDARD; PRT; 131 AA.
PS1466; O9UEA2;
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Leydig insulin-like peptide precursor (Ley-I-L) (Relaxin-like factor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,
Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Ilu S.,
Attix C., Andrelse T., Trankheim M., Amico-Keller G., Coefield J.,
Duartes S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
Arellano A., Saunders C., Ow D., Nolan M., Trong S., Kobayashi A.,
Olsen A.S., Carrano A.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Testis;
MEDLINE=44307715; PubMed=8034302;
MEDLINE=43307715; PubMed=8034302;
MINIMITE E., Adham I.M., Hobohm U., Murphy D., Sander C., Engel W.;
"A human cDNA coding for the Leydig insulin-like peptide (Ley I-L).";
Hum. Genet. 94:91-94(1994).
                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Structural organization of the porcine and human genes coding for Exydig cell-specific insulin-like peptide (LEY I-L) and chromosomal localization of the human gene (INSL3)."; Genomics 20:13-19(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence analysis of an ~700 kb region in 19p13.1 between JAK3 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                               INSULIN-LIKE PEPTIDE INSLS B CHAIN (POTENTIAL).
                                                                                                 INSULIN-LIKE PEPTIDE INSL5 A CHAIN
                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Burkhardt E., Adham I.M., Brosig B., Gastmann A., Mattei M.-G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULEIDE BONDS (EX SIMILARITY).
-!- SUBCELLUAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN PRENATAL, AND POSTNATAL LEYDIG CELLS. FOUND AS WELL IN THE CORPUS LUTEUM, TROPHOBLAST, FETAL MEMBRANES AND BREAST.
                                                                                 CONNECTING PEPTIDE (POTENTIAL)
                                                                                                                                                                                                                             54.7%; Score 82; DB 1; Length 135; 66.7%; Pred. No. 1.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                           Pred. No. 1.9e-05;
;; Mismatches 5; Indels
                                                                                                                               INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                              BY SIMILARITY.
98FFCB20E9C4BC1F CRC64;
                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                  (POTENTIAL)
                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE-94292172; PubMed-8020942;
                 Insulin family; Hormone; Signal.
                                                                                                                                                                               15318 MW;
                                                                                                                                                                                                                                                                                         7 VRLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                             26 VRLCGLEYIRTVIYICASSRW 46
PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                             Conservative
                                                 48
                                                                              114
                                                                                                                               122
                                                                                                                                                            121
135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPERMATOGENESIS.
                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                        19
                                                                              49
115
                                                                                                                            29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INSL3 OR RLF.
                                                                                                                              DISULFID
                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Engel W.;
 PROSITE;
                                                                                                                                               DISULFID
                                                                                                                                                            DISULFID
                                  SIGNAL
                                                                              PROPEP
                                                 CHAIN
                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                          INL3_HUMAN
                                                                                                                                                                                                                                                                                                                                                                       RESULT
ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Leydig insulin-like peptide precursor (Ley-I-L) (Relaxin-like factor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adham I.M., Burkhardt E., Benahmed M., Engel W.; "Cloning of a cDNA for a novel insulin-like peptide of the testicular Leydig cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Structural organization of the porcine and human genes coding for a Leydig cell-specific insulin-like peptide (LEY I-L) and chromosomal localization of the human gene (INSL3)."; Genomics 20:13-19(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPERMATOGENESIS.
-!- SUBINIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO DISULFIDE BONDS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                               C PEPTIDE (POTENTIAL).
LEXDIG INSULIN-LIKE PEPTIDE A CHAIN.
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sus scrofa (Pig).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                       LEYDIG INSULIN-LIKE PEPTIDE B CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-94292172; PubMed-8020942;
Burkhardt E., Adham I.M., Brosig B., Gastmann A., Mattei M.-G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.7%; Score 76; DB 1; Length 131; 55.0%; Pred. No. 0.00015; Live 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                -> T (IN REF. 3).
C5799D610424C136 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 AA.
                                                                                                                                                                                                          InterPro; IPR000739; Insulin_IGF_relaxin.
Pfam; PF00049; Insulin; 1.
SMART; SM00078; IIGF; 1.
                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biol. Chem. 268:26668-26672(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                 CAA52017.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Testis;
MEDLINE=94075362; PubMed=8253799;
                                                                                                                                                                                                                                                                       Insulin family; Hormone; Signal
                                                                                                                                                               EMBL; X73637; CAA52017.1; ALL.
EMBL; AC005952; AAC72277.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                               14472 MW;
                                                                                                                                                                                                                                                          PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 RLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 KLCGHHFVRALVRVCGGPRW 51
                                                                                                                                                    EMBL; S72482; AAB31371.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                     55
104
131
116
129
120
60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                              MIM; 146738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INSL3 OR RLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INL3_PIG
P51461;
                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Engel W.;
                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                    PROPEP
                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INL3_PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
ά
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rissue-Colon;
                                                                                                                                                                                                                                                                                                                                                                                        INL5_MOUSE
Q9WUG6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hsu S.Y.;
                                                                                                                                                                         DISULFID
                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                  PROPEP
                                                                                                                         SIGNAL
                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                           INL5_MOUSE
                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                      δλ
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is non oway modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               077801;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Leydig insulin-like peptide precursor (Ley-I-L) (Relaxin-like factor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bathgate R.A.D., Balvers M., Hunt N., Ivell R.; "Relaxin-like factor gene is highly expressed in the bovine ovary of the cycle and pregnancy: sequence and messenger ribonucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO DISULEDIDE BONDS (BY SIMILARITY).
-!- TISSUE SPECIFICITY: EXPRESSED EXCLISIVELY IN LEYDIG CELLS.
-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                   POTENTIAL.
LEYDIG INSULIN-LIKE PEPTIDE B CHAIN.
C PEPTIDE (POTENTIAL).
LEYDIG INSULIN-LIKE PEPTIDE, A CHAIN.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN PRENATAL AND POSTNATAL LEYDIG CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol, Reprod. 55:1452-1457(1996).
                                                                                                                                                                                                                                                                                                                                                                             Score 75; DB 1; Length 131;
Pred. No. 0.00021;
; Mismatches 5; Indels
                                   -1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                         8AB718870859EF3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132 AA
                                                                                                                                                                                                                                                                                                                              SIMILARITY
                                                                                                                                                                                      Interpro; IPR000739; Insulin_IGF_relaxin.
Pfam; PF00049; Insulin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Testis;
MEDLINE=97107158; PubMed=8949906;
                                                                                                                                                                                                                                          Insulin family; Hormone; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                       4;
                                                                                                                                                                                                                                                                                                                                                                              50.0%;
                                                                                                                                                                                                                                                                                                                                            ×.
                                                                                                                                                                EMBL; X73636; CAA52016.1; -.
                                                                                                                                                                                                               SMART; SM00078; IlGF; 1.
PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                               8 RLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                            32 KLCGHHFVRALVRLCGGPRW 51
                                                                                                                                                                                                                                                      24
56
103
131
116
129
120
                                                                                                                                                                           CAA48449.1;
                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Ce<sup>°</sup>
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPERMATOGENESIS.
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 11; Conserva
                                                                                                                                                                                                                                                                                                                46 1
115 1
131 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9913;
                                                                                                                                                                           EMBL; X68369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INSL3 OR RLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INL3_BOVIN
                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                             PROPEP
                                                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INL3_BOVIN
```

```
Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                           (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lok S., Jaspers S.; "Identification of INSL5, a new member of the insulin superfamily."; Genomics 60:50-56(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conklin D., Lofton-Day C.E., Haldeman B.A., Ching A., Whitmore T.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning of two novel mammalian paralogs of relaxin/insulin family proteins and their expression in testis and kidney."; Mol. Endocrinol. 13:2163-2174(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                              C PEPTIDE (POTENTIAL).
LEYDIG INSULIN-LIKE PEPTIDE A CHAIN.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                      LEYDIG INSULIN-LIKE PEPTIDE B CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Insulin-like peptide INSLS precursor (Insulin-like peptide 5)
(Relaxin/insulin-like protein) (Relaxin/insulin-like factor 2).
INSLS OR ZINS3 OR RIF2 OR RIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.0%; Score 75; DB 1; Length 132; 55.0%; Pred. No. 0.00021; Live 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A5585500C7F2241D CRC64;
modified and this statement is not removed. entities requires a license agreement (See h or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY
                                                                                                                                InterPro; IPR000739; Insulin_IGF_relaxin.
Pfam; PF00049; Insulin; 1.
SMART; SM00078; IlGF; 1.
                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=FVB; TISSUE=Ovary;
MEDLINE=20065648; PubMed=10598589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Colon;
MEDLINE-99389725; PubMed=10458910;
                                                                                                                                                                                                                                       Insulin family; Hormone; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Created)
                                                                                                       EMBL; AF094580; AAC63380.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    14378 MW;
                                                                                                                                                                                                         PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 RLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 KLCGHHFVRALVRLCGGPRW 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 50.0%
Best Local Similarity 55.0%
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
```

```
between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Placenta, and Ovary,
MEDLINE-96328899; pubMed=8735594;
MEDLINE-96328899; pubMed=8735594;
Gunnersen J. M., Fu P., Roche P.J., Tregear G.W.;
"Expression of human relaxin genes: characterization of a novel
alternatively-rpliced human relaxin mRNA species.";
Mol. Cell. Endocrinol. 118:85-94(1996).
-! FUNCTION: RELAXIN IS AN OVARIAN HORMONE THAT ACTS WITH ESTROGEN TO
PRODUCE DILARATION OF THE BITHT CANAL IN MANY MAMMALS. MAY BE
INVOLVED IN REMOBELING OF CONNECTIVE TISSUES DUBING PREGRANCY,
PROMOTING GROWTH OF PUBIC LIGAMENTS AND RIPENING OF THE CERVIX.
-! SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                             (POTENTIAL).
CONNECTING PEPTIDE (POTENTIAL).
INSULIN-LIKE PEPTIDE INSL5 A CHAIN
                                                                                                                                                                                                                                                                                INSULIN-LIKE PROTEIN INSL5 B CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 2), AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Evans B.A., Fu P., Tregear G.W.; "Characterization of two relaxin genes in the chimpanzee."; J. Endocrinol. 140:385-392(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 75; DB 1; Length 135;
Pred. No. 0.00022;
5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                         INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                      05FF9A0F613DBF92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Mismatches
                                                                                                                                                                                    MGD; MGI:1346085; Insl5.
InterPro; IPR000739; Insulin_IGF_relaxin.
SMART; SM00078; IlGF; 1.
                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                         EMBL; AF076971; AAD48089.1; --
EMBL; AF054841; AAF09093.1; ALT_INIT.
EMBL; BC010968; AAH10968.1; --
EMBL; BC010968; AAH10968.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prorelaxin H2 precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94238260; PubMed=8182365;
                                                                                                                                                                                                                                                  Insulin family; Hormone; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF133817; AAD29687.1; -.
                                                                                                                                                                                                                                  PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                      15524 MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 VRLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 VKLCGLDYVRTVIYICASSRW 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pan troglodytes (Chimpanzee).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.0%;
52.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Conservative
                                                                                                                                                                                                                                                                                                           114
                                                                                                                                                                                                                                                                                                                                                                                    126
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                   121
135 AA;
                                                                                                                                                                                                                                                                                                         49
115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNL2 OR RLX2
                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PARTIAL
                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                           PROPEP
                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
REL2_PANTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
 Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
```

-!- SUBCELLULAR LOCATION: Secreted

```
the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HVSLGISPDGGKALRIGSCFTREFLGALS (IN ISOFORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
            produced by alternative splicing.
--- TISSUE SPECIFICITY: EXPRESSED IN THE CORPUS LUTEUM OF PREGNANCY AND IN THE PLACENTA.
---- SIMILARITY: BELONGS TO THE INSULIN/IGE/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                             PROSITE; PS00262; INSULIN; 1.
Insulin family; Hormone; Multigene family; Signal; Polymorphism;
Alternative splicing.
-!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
                                                                                                                                                                                                                                                                                                                                                                                                               EIVPSFINKDTETINMMSEFVANLPQELKLTLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MISSING (IN ISOFORM 2).

KSTWS -> MSTLG (IN SOME ALLELES).
220851E3134CEBDB CRC64;
                                                                                                                                                                                                                                                                                                                     POTENTIAL.

RELAXIN B CHAIN (PROBABLE).
CONNECTING PEPTIDE (PROBABLE)
RELAXIN A CHAIN (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 72; DB 1; Length 166;
Pred. No. 0.00075;
3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                       INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-077-1996 (Rel. 34, Created)
01-077-1996 (Rel. 34, Last sequence update)
16-077-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                         InterPro; IPR000739; Insulin_IGF_relaxin.
Pfam; PF00049; Insulin; 1.
SMART; SM00078; IlGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prorelaxin Hi precursor (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94238260; PubMed=8182365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 K
18760 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 IKLCGRELVRAQIAICGKSTW 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 VRLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                     EMBL; 227245; CAA81758.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 57.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pan troglodytes (Chimpanzee)
                                                                                                                                                                                                 EMBL; S83209; AAD14430.1;
HSSP; P04090; 6RLX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                  34
1138
1166
1153
1166
1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                     85 1
30
166 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNL1 OR RLX1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REL1_PANTR
P51454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                      NON_TER
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                               VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                               CHAIN
PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
REL1_PANTR
                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
```

. 0

```
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hudson P., John M., Crawford R., Haralambidis J., Scanlon D., Gorman J., Tregear G., Shine J., Niall H.; Relaxin gene expression in human ovaries and the predicted structure of a human preprorelaxin by analysis of cDNA clones."; EMBO J. 3:2333-2339(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-83141755; PubMed=6298628;
Hudson P., Haley J., John M., Cronk M., Crawford R., Haralambidis J.,
Tregear G., Shine J., Niall H.,
"Structure of a genomic clone encoding biologically active human
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
            -:- SUBCELLUIAR LOCATION: Secreted.
-:- TISSUE SPECIFICITY: EXPRESSED IN THE CORPUS LUTEUM OF PREGNANCY BUT NOT IN THE PLACENTA.
-:- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarfilini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                           RELAXIN B CHAIN (PROBABLE).
CONNECTING PEPTIDE (PROBABLE).
RELAXIN A CHAIN (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                47.3%; Score 71; DB 1; Length 166; 57.1%; Pred. No. 0.0011;
                                                                                                                                                                                                                                                                                                                                                     INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 0.0011;
3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                           7F469B1FB9259F4F CRC64;
                                                                                                                                                                                                        Interpro; TPR00073; Insulin_IGF_relaxin.
Pfam: PPF00049; Insulin; 1.
SMART; SM00078; IIGF; 1.
PROSITE; PS00262; INSULIN; 1.
Insulin family; Hormone; Multigene family; Signal.
NON_TER 1 5 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RELL_HUMAN STANDARD; PRT; 185 AA. P04808; 099936; 13-AuG-1987 (Rel. 05, Created) 13-AuG-1987 (Rel. 05, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Prorelaxin H1 precursor.
                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=85051298; PubMed=6548702;
                                                                                                                                                                                                                                                                                                                                                                              BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 IKLCGRELVRAQIAICGMSTW 33
                                                                                                                                                                                                                                                                                                                                                                                             18730 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 VRLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                       EMBL; 227225; CAA81739.1; -. HSSP; P04090; 6RLX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 301:628-631(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 57.1
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             166 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sehra H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              relaxin.
                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                             CHAIN
PROPEP
                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REL1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its modified morphofit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LQQYVP -> GDFIQTVSLGISPDGGKALRTGSCFTREFLG
ALSKLYHPSSTKIQKL (IN ISOFORM 2).
MISSING (IN ISOFORM 2).
                                                                                                                                                                                                                                                                            TISSUE-Prostate;
MEDLINE-96128899; PubMed=8735594;
MEDLINE-96128899; PubMed=8735594;
MEDLINE-96128899; PubMed=8735594;
MEDLINE-96128899; PubMed=8735594;
MEDLINE-96128899; PubMed=8735594;
MEDLINE-118:85-94(1996).
MEDLINE-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARIȚY.
EIVPSFINKDTETIIMLEFIANLPPELKAALSERQPSLPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- SUBCELLULAR LOCATION: Secreted.
-i- ALTERNATIVE PRODUCTS: 2 isoforms: 1 (shown here) and 2; are produced by alternative splicing.
-i- TISSUE SPECIFICITY: Prostate. Not expressed in placenta, decidua
                                                                                                                                                                                                  PARTIAL SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RELAXIN B CHAIN (PROBABLE).
CONNECTING PEPTIDE (PROBABLE).
RELAXIN A CHAIN (PROBABLE).
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or ovary.
-!- MISCELLANEOUS: H1 RELAXIN MAY BE A PSEUDOGENE.
-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                    Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               K -> M (IN DBSNP:618066).
/FTId=VAR_011962.
B318628ABFEC7142 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00262; INSULIN: 1.
Insulin family; Hormone; Multigene family; Signal;
Alternative splicing; Polymorphism.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro; IPR000739; Insulin_IGF_relaxin.
Pfam; PF00049; Insulin; 1.
PRINTS; PR00276; INSULINA.
SMART; SM00078; IIGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X00949; CAA25461.1; EMBL; V00578; CAA23839.1; EMBL; V00577; CAA23838.1; EMBL; A06926; CAA00603.1; EMBL; A07364; CAA00599.1; EMBL; A17329; CAA01325.1; EMBL; A17329; CAA01325.1; EMBL; BC005956; AAH05956.1; -
SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21145 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S83200; AAD14429.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158
185
172
185
185
1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185
28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A44559; A44559.
HSSP; P04090; 6RLX.
MIM; 179730; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFIDE BONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118
28
                                               TISSUE-Prostate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23
56
163
35
47
                                                                                      Strausberg R.;
                                                                                                                                                                                                                                                      SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOPORM 1), AND TISSUE SPECIFICITY.
MEDLINE-85051298; PubMed-6548702;
Hudson P., John M., Crawford R., Haralambidis J., Scanlon D.,
Gorman J., Tregear G., Shine J., Niall H.;
"Relaxin gene expression in human ovaries and the predicted structure
of a human preprorelaxin by analysis of cDNA clones.";
EMBO J. 3:2333-2339(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "X-ray structure of human relaxin at 1.5 A. Comparison to insulin and implications for receptor binding determinants.";
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Winslow J.W., Shih A., Bourell J.H., Weiss G., Reed B., Stults J.T., Goldsmith L.T., "Human seminal relaxin is a product of the same gene as human luteal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Buellesbach E.E., Schwabe C.; "Total synthesis of human relaxin derivatives by solid-phase peptide synthesis and site-directed chain combination."; J. Biol. Chem. 266:10754-10761(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                    ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gunnersen J.M., Fu P., Roche P.J., Tregear G.W.;
"Expression of human relaxin genes: characterization of a novel alternatively-spliced human relaxin mRNA species.";
Mol. Cell. Endocrinol. 118:85-94(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Winslow J.W., Griffin P.R., Rinderknecht E., Vandlen R.L.; "Structural characterization by mass spectrometry of native and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PARTIAL SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92015205; PubMed=1656049;
Eigenbrot C., Randal M., Quan C., Burnier J., O'Connell L.,
Rinderknecht E., Kossiakoff A.A.;
Score 71; DB 1; Length 185;
Pred. No. 0.0012;
3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sehra H.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blomed. Environ. Mass Spectrom. 19:655-664(1990).
                                                                                                                                                                                                                                                                                                                                   RELZ_HUMAN STANDARD; PRT; 185 AA. P04090; O9UCX3; O99936; O1-NOV-1986 (Rel. 03, Created) 01-NOV-1986 (Rel. 03, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-96328899; PubMed-8735594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Endocrinology 130:2660-2668(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91250367; PubMed=2040595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92241162; PubMed=1572287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=91167739; PubMed=2076464;
                                                          3;
                                                                                                                                                         32 IKLCGRELVRAQIAICGMSTW 52
                                                                                                                  7 VRLCGREFIRAVIFTCGGSRW 27
47.38;
57.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 25-53 AND 162-185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       recombinant human relaxin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PARTIAL SEQUENCE OF 25-51.
                                                       12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prorelaxin H2 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Prostate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Semen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYNTHESIS.
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      relaxin.
                                                                                                                                                                                                                                                                                                         REL2_HUMAN
                                                    Matches
                                                                                                                                                                                g
                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                         THE SECTION OF THE SECTION OF SEC
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EIVPSFINKDTETINMMSEEVANLPOELKLTLSEMOPALPO
LOOHVP -> GDFIQTVSLGISPDGGKALRTGSCFTREFLG
ALSKLCHPSSTKIQKP (IN ISOFORM 2).
                                                                                                       -!- SUBCELLULAR LOCATION: Secreted.
-!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are produced by alternative splicing.
-!- TISSUE SPECIFICITY: Expressed in the ovary during pregnancy. Also expressed in placenta, decidua and prostate.
-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
J. Mol. Biol. 221:15-21(1991).

-!- FUNCTION: RELAXIN IS AN OVARIAN HORMONE THAT ACTS WITH ESTROGEN PRODUCE DILATATION OF THE BIRTH CANAL IN MANY MAMALE. MAY BE INVOLVED IN REMODELING OF CONNECTIVE TISSUES DURING PREGNANCY.

PROMOTING GROWTH OF PUBIC LIGAMENTS AND RIPENING OF THE CERVIX.

-!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PROUGES; INCULIN; I.
Insulin family; Hormone; Multigene family; Signal; 3D-structure; Alternative splicing.

Alternative splicing.

SIGNAL
25 53 CONDECTION PEPTIDE.
CHAIN
25 157 CONDECTION PEPTIDE.
CHAIN
MOD_RES 162 162 PYRROLIDONE CARBOXYLIC ACID.
DISULEID 35 172 INTERCHAIN.
DISULEID 35 172 INTERCHAIN.
DISULEID 171 176 EIVPSFINKOFFINMASEFVANLPOEIKLTLSEMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.3%; Score 71; DB 1; Length 185; 57.1%; Pred. No. 0.0012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21042 MW; AC73DBDE2090091B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISSING (IN ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                105 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000739; Insulin_IGF_relaxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                      EMBL; X00948; CAA25460.1; -. BMBL; AL135786; CAC04177.1; -. EMBL; AL135786; CAC04176.1; -. EMBL; S83200; AAD14429.1; -. EMBL; A17315; CAA01324.1; -. EMBL; A06925; CAA01324.1; -. PIR; A60925; A60982.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 VRLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00049; Insulin; 1.
SMART; SM00078; IIGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                               PDB; 6RLX; 31-OCT-93.
MIM; 179740; -.
                                                                                           DISULFIDE BONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163
174
176
178
183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARSPLIC
HELIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INL3_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9WUKO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HELIX
TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HELIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HELLX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INL3_RAT
ID INL3.
AC Q9WUI
    ŏ
```

```
STRAIN=129/SVJ;
Zimmermann S.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INL3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mack by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INL3_CALJA STANDARD; PRT; 131 AA.
097937; 097938;
16-02T-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last insolution update)
16-0CT-2001 (Rel. 40, Last insolution update)
16-0CT-2001 (Relaxin-like factor).
                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                     -!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Callithrix jacchus (Common marmoset).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C PEPTIDE (POTENTIAL).
LEXDIG INSULIN-LIKE PEPTIDE A CHAIN.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEYDIG INSULIN-LIKE PEPTIDE B CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                       DISULFIDE BONDS (BY SIMILARITY).
--- SUBCELLULAR LOCATION: Secreted.
--- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN LEYDIG CELLS.
--- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                 Spiess A.-N., Pusch W., Ivell R., "Cloning and sequence of the rat relaxin-like factor and its
 16-OCT-2001 (Rel. 40, Created)
LoCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Leydig insulin-like peptide (Ley-I-L) (Relaxin-like factor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.7%; Score 70; DB 1; Length 105; 50.0%; Pred. No. 0.00096; trive 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                    Submitted (MAR-1999) to the EMBL/Genbank/DDBJ databases.
-!- FUNCTION: COULD PLAY A ROLE IN TESTICULAR FUNCTION AND SPERMATOGENESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              903716A8FBEB13EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF139918; AAD33663.1; -.
InterPro; IPR000739; Insulin_IGF_relaxin.
Pfam; PF00049; Insulin; 1.
PRART; SR000708; IIGF; 1.
PROSTIE; PS00262; INSULIN; 1.
Insulin family; Hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77 C
105 LE
90 IN
103 IN
94 BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 RLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 KLCGHHLVRALVRVCGGPRW 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 50.0 tes 10; Conservative
                                                                                                                                                                                                       STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
18
89
105 /
                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9483;
                                                                                                                                                   NCBI_TaxID=10116;
                                                                                      INSL3 OR RLF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Callithrix.
                                                                                                                                                                                                                                                          promotor."
                                                                      (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON_TER
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INL3_CALJA
```

SOURCE STATES SEED BEST STATES SEED BEST SEED

ŏ

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INL3_MOUSE STANDARD, PRT; 122 AA.
009107; P97744; STANDARD, OR1.NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 34), Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
1-Eydig insulin-like peptide precursor (Ley-I-L) (Relaxin-like factor).
INSI3 OR RE.
Mus musculus (Mouse).
SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE=99115234; PubMed=9916013;
Zarreh-Hoshyari-Khah M., Einspanier A., Ivell R.;
"Differential splicing and expression of the relaxin-like factor gene in reproductive tissues of the marmoset monkey (Callithrix jacchus).";
Biol. Reprod. 60:445-453(1999).
-i. FUNCTION: COULD PLAY A ROLE IN TESTICULAR FUNCTION AND
                                                                                                                                                                                                                                                                                                                                                                         SHORT/TRUNCATED FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                   -:- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO DISULFIDE BONDS (BY SIMILARITY).
-:- SUBCELLULAR LOCATION: Secreted.
-:- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
LEYDIG INSULIN-LIKE PEPTIDE B CHAIN.
C PEPTIDE (POTENTIAL).
LEYDIG INSULIN-LIKE PEPTIDE A CHAIN.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
GELLOWLERRH -> ESHSAAQDGGQ (IN SHORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.0%; Score 69; DB 1; Length 131; 50.0%; Pred. No. 0.0017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MISSING (IN SHORT ISOFORM). 685743CAEECF8731 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insulin family; Hormone; Signal; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR000739; Insulin_IGF_relaxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISOFORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AJ011961; CAA09888.1; -.
EMBL; AJ011962; CAA09888.1; JOINED.
EMBL; AJ011961; CAA09889.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14252 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00049; Insulin; 1.
SMART; SM00078; I1GF; 1.
PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 KLCGHHFVRALVRVCGGPLW 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 RLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104
131
117
130
121
74
                                                                                                                                                                                                                                      SPERMATOGENESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P01315; 1ZEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
```

ö

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                           A KOSKIMIAL 29/5VJ;

XX MEDLINE-98088907; PubMed-9428631;

XX MSDLINE-98088907; PubMed and its promoter are located at a vithin the 3' region of the JAK3 genomic sequence.";

XX The mouse relaxin-like factor gene and its promoter are located at a vithin the 3' region of the JAK3 genomic sequence.";

XX THE SERVATION: COULD PLAY A ROLE IN TESTICULAR FUNCTION AND SPERMATOGENESIS.

CC -1- SUBNINIT: HETERODINER OF A B CHAIN AN A CHAIN LINKED BY TWO CC DISULFIDE BONDS (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: SECRETEGE.

CC -1- SUBCELLULAR BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.

CC -1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.

CC -1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                             Pusch W., Balvers M., Ivell R.; "Molecular cloning and expression of the relaxin-like factor from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.

LEYDIG INSULIN-LIKE PEPTIDE B CHAIN.

C PEPTIDE (POTENTIAL).

LEYDIG INSULIN-LIKE PEPTIDE A CHAIN.

INTERCHAIN (BY SIMILARITY).

INTERCHAIN (BY SIMILARITY).

BY SIMILARITY.

P -> T (IN REF. 1).

VETRO -> CGDPG (IN REF. 1).
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A -> S (IN REF. 1).
QRQRR -> HARG (IN REF. 1)..
10783AB4896CF103 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; S82815; AAB39365.1; --
EMBL; AF136524; AAD4585.1; --
MGD; MG108427; Ins13.
InterPro; IPR000739; Insulin_IGF_relaxin.
SMART; SW00078; IlGf; 1.
PROSITE; PS00262; INSULIN; 1.
Insulin family; Hormone; Signal.
                                                                                                                                                Endocrinology 137:3009-3013(1996).
                                                        TISSUE=Testis;
MEDLINE=96366811; PubMed=8770925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13586 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X95603; CAA64861.1; -.
                                       SEQUENCE FROM N.A.
                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                mouse testis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
```

:||| :| :| || || 27 KLCGHHLVRTLVRVCGGPRW 46 8 RLCGREFIRAVIFTCGGSRW 27

ŏ g

ö

0; Gaps

Ouery Match
Best Local Similarity 45.0%; Pred. No. 0.0044;
Matches 9; Conservative 4; Mismatches 7; Indels

Search completed: June 27, 2002, 16:16:52 Job time: 486 sec

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

June 27, 2002, 16:16:28 ; Search time 58.57 Seconds (Without alignments) 79.748 Million cell updates/sec Run on:

1 RAAPYGVRLCGREFIRAVIFTCGGSRW 27 US-09-781-077-2_COPY_26_52 150 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

562222 seqs, 172994929 residues Searched:

562222 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SPTREMBL_19:*

1: Sp_archea:*
2: sp_bacteria:*
3: Sp_fung1:*
4: Sp_human:*
5: Sp_invertebrate:*
5: Sp_mammal:*
5: Sp_mammal:*
5: Sp_mhc:*
5: Sp_organelle:*
5: Sp_organelle:*
5: Sp_organelle:*
5: Sp_organelle:*
5: Sp_organelle:*
5: Sp_organelle:* sp_virus:*
sp_vertebrate:*
sp_unclassified:* sp_plant:* sp_rodent:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_rvirus:*
sp_bacteriap:*

sp_archeap:*

SUMMARIES

	Description		Obushe bene carion					Vynuze capra hircu	Q28429 gorilla gor	Q9n0f2 equus cabal	Odmvka felic cilvo	CONTRO TELLS SILVE	October Sapin		09trg5 sus scrofa	028782 nongo pagma	-	Cazaya rrankia sp.	094ss5 danaceticht	Q9vfk9 drosophila
1	ID	09DEP8	одприб	STONEO	09GK47	028431	TOPONO ODONO	028420	0.204.29	CANOF.Z	29MYK8	028788	O LONGO		JYT RG5	028782	7925V5		294555	29VFK9
	DB	13	4	و ا	ی ر	ى د				0	ဖ	9	۷		0	9	ď	10	0	S.
	Query Match Length DB	155	65	131	131		131	1 6	1 0	2	180	33	199	1	7	33	494	613	710	941
ф	Query	69.3	50.7	50.0	50.0	47.3	44.7	42.0	10		40.7	38.0	38.0	36 7		36.0	34.3	27.0		34.0
	Score	104	9/	75	75	71	67	63	61	5.5	19	57	57	η. Γ) :	54	51.5	5	1 1	77
	Result No.	1	7	e	4	S	9	7	α	0 0	ָּ ת	10	11	12	3 6	£1.	14	ŗ	1 -	9 T

ö

6 GVRLCGREFIRAVIFTCGGSRW 27 |:|||||:|||| |: :||||||| 29 GIRLCGRDFIRTVVMSCGGSRW 50

δλ qq

	=	3	_		_			_	,		æ	1																
pantoea agg	in in Stime Stime	taenonvala	dallus dall	or seixeles	gallus gall		homo sanien	mus musculu	shiqella fl	escherichia	arabidopsis				qalaxias de			galaxias sp		- 0	ja	ralaxias fa			Q		homo sapien	ı
Q52064 Q28780	099k±9	057687	P79890	095999	092010	000403		9	O9xci4		9	091hr4	0921r3		-	Q959a7										-	Q9blr0 P	
																												Š
Q52054 Q28780	Q99KT9	057687	P79890	Q959B9	092010	000403	043829	008376	Q9XCI4	Q93K84	Q9M1L9	Q91HR4	Q921R3	Q9T9H1	095823	Q959A7	Q958Y4	Q958Y3	095901	Q9MKJ1	оэмкло	Q959C5	Q959B1	09TA02	047815	096383	Q9B1R0	S THAT S THE S THE S
v v	11	13	13	œ	13	4	4	11	7	7	10	12	11	œ	œ	8	ထ	ထ	8	œ	œ					æ	8	
45/	88	187	187	398	448	449	449	449	235	284	372	555	334	551	156	250	365	368	397	412	412	471	520	598	599	602	603	
33.3	ė	m	m	m	m	e	m.		ė	m.	e.	ë.	ď	ď	ď	ď	~;	~	Α.	~:	~:	~:	٠.	~;	~;	~i	٠.	
50	20	20	20	20	20	20	20		49.5	U١	O١	O1	49	49	48	48	48	48	48	48	48	48	48	48	48	48	48	
18	19	20	21	22	23	24	25	76	27	28	29	30	31	32	33	34	3.5	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

	e) late)	ata; Euteleostomi; dea; Ranidae; Rana.	er of the rog Rana esculenta." TY) XIN FAMILY.	Length 155;
PRT: 155 AA.	Created) Last sequence update) Last annotation update)	Rana esculenta (Edible frog). Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; CDFI_TaxID=8401;	SEQUENCE FROM N.A. SEQUENCE FROM N.A. TISSUE=TESTIS; MEDINE=21309007; PubMed=11416046; MEDINE=21309007; PubMed=11416046; MEDINE=21309007; PubMed=11416046; MEDINE=21309007; PubMed=11416046; "Isolation and characterization of a novel member of the relaxin/insulin family from the testis of the frog Rana estandorinology 142:3231-3238(2001). -! SUBCELLUAR LOCATION: SECRETED (BY SIMILARITY). -! SIMILARITY BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY. InterPro; IPR000739; Insulin_IGF_relaxin. InterPro; IPR000252; N6_Mtase. FFAM: PR00049; Insulin; 1. SMART; SW00078; IIGF; 1. PROSITE; PS00092; N6_MTASE; UNKNOWN_1.	Score 104; DB 13;
PRELIMINARY;	(TrEMBLrel. 16, (TrEMBLrel. 16, (TrEMBLrel. 19, E PROTEIN.	Rana esculenta (Edible frog). Eukaryota, Metazoa; Chordata; Amphibia; Batrachia; Anura; N NCBI_TaxID=8401;	SEQUENCE FROM N.A. TISSUE=TESTIS; MEDLINE=21309007; PubMed=11416046; MEDLINE=21309007; PubMed=11416046; MEDLINE=21309007; PubMed=11416046; MEDLINE=21309007; PubMed=11416046; "Isolation and characterization of a nove relaxin/insulin family from the testis of 1-1 SUBCELLULAR LOCATION: SECRETED (BY SIMILARIY: BELONGS TO THE INSULIN/IG EMBL; AJ298874; CAC16108.1; -1. InterPro; IPRO0073; Insulin; 1. PFAM: PRO0049; Insulin; 1. PROSITE: PS00092; NG_MTASE; UNKNOWN_1. SEQUENCE 155 AA; 17470 MW; S17ADAS385	69.38;
RESULT 1 Q9DEP8 ID Q9DEP8	Q9DEP8; 01-MAR-2001 (TrEMBLre 01-MAR-2001 (TrEMBLre 01-DEC-2001 (TrEMBLre RELAXIN-LIKE PROTEIN.	Enhana esculenta (Eukaryota; Metaz Amphibia; Batrac NCBI_TaxID=8401;	SEQUENCE FROM N.A. TISSUE-FESTIS; MEDLING-2130907; DE Rienzo G., Anie m'Isolation and charalin/insulin fa Endocrinology 142: -1 - SIMILARITY: BE EMBL; AJ298874; CA InterPro; IPR00073 I	Query Match

32 KLCGHHFVRALVRLCGGPRW 51

= ::=:-, =::

```
4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
Q28431
                                              RESULT
                                                                         Q9GK47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-20155568; PubMed=10687860;
Hombach-Klonisch S., Kauffold J., Rautenberg T., Steger K., Tetens F.,
Fischer B., Klonisch T.;
                                                                                                                                                                                                                                                                                                                                            lamerdin J.E., McCready P.M., Skowronski E., Scott D.,
Burkhart-Schultz K., Gordon L., Dias J., Sakaldasis G., Stilwagen S.,
Bhan H., Velasco N., Do L., Regala W., Terry A., Danganan L.,
Erler A., Christensen M., Georgescu A., Avila J., Attix C.,
Andreise T., Amico-Keller G., Coefield J., Duarte S., Lucas S.,
Bruce R., Thomas P., Quan G., Krommiller B., Arellano A., Sanders C.,
Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.S., Carrano A.V.;
Sequence analysis of a 5.7 Mb region in 19p13.1.",
Sequence analysis of the EMBL/GenBank/DDBJ databases.
EMBL, AC007201, AD22740.1;
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoldea;
Cervidae; Cervinae; Cervus.
                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Relaxin-like factor (RLF) mRNA expression in the fallow deer."; Mol. Cell. Endocrinol. 159:147-158(2000).
-! SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
-! SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 50.0%; Score 75; DB 6; Length 131; Best Local Similarity 55.0%; Pred. No. 0.00075; Matches 11; Conservative 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 50.7%; Score 76; DB 4; Length 65; Best Local Similarity 55.0%; Pred. No. 0.00026; Matches 11; Conservative 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 AA; 14406 MW; EC7731679E60B0C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 AA; 7088 MW; 9D0BF767161DE030 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
RELAXIN-LIKE PROTEIN.
                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 131 AA.
                                                 65 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interpro; IPR000739; Insulin_IGF_relaxin.
SMART; SM00078; IlGF; 1.
PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dama dama (Fallow deer) (Cervus dama).
                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF254740; AAF67742.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 KLCGHHFVRALVRVCGGPRW 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 RLCGREFIRAVIFICGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                   PRELIMINARY;
                                                                                                                                                                                 INL3_HUMAN (FRAGMENT).
                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=30532;
                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09N0T8;
                                                                               09прн6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9N0T8
                                                 9нап60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 m
  ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
Q9N0T8
RESULT
Q9UPH6
                                                      SOUR SEASON SOUR SOUR SEASON S
```

8 RLCGREFIRAVIFTCGGSRW 27

δλ

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                     TISSUE=TESTIS; Klonisch T., Tetens F., Fischer B., Hombach-Klonisch S.; "Molecular remodeling of members of the relaxin family during primate
                                                                                                                                         Galago crassicaudatus (Thick-tailed galago) (Otolemur crassicaudatus).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Strepsirhini; Galagonidae; Otolemur.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gorilla gorilla (gorilla).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50.0%; Score 75; DB 6; Length 131; 55.0%; Pred. No. 0.00075; ive 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                       MOI. BIOI. EVOI. 0:0-0(2001).
-!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
EMBL; AF317624; AAG42317.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.3%; Score 71; DB 6; Length 33; 57.1%; Pred. No. 0.00073; tive 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR000739; Insulin_IGF_relaxin.
SMART; SM0078; IlGF; 1.
PROSITE; PS00262; INSULIN; 1.
SEQUENCE 131 AA; 14414 MW; F18AFA9ACFC85943 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER 1 1 1 SEQUENCE 33 AA; 3766 MW; 54BE68D028EDA2F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Evans B.B.A., Fu P., Tregear G.G.W.;
"Characterisation of primate relaxin genes.";
J. Mol. Endocrinol. 0:0-0(1993).
HSSP; P04090; 6RLX.
PRT; 131 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B IKLCGRELVRAQIAICGMSTW 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 VRLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 RLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 KLCGHHFVRALVRLCGGPRW 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 55.09
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
  PRELIMINARY;
                                                                                                                            RELAXIN-LIKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RELAXIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9593;
                                                                                                                                                                                                                           NCBI_TaxID=9463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-RG 287;
                                                                                                                                                                                                                                                                                                                                                                          evolution.";
                       Q9GK47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  028431
  09GK47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

ö

```
6
                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
Q9MYK8
                                                                                                             Q9N0F2
                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                      MEDLINE-99260294; Pubmed-10331451;
Monbach-Klonisch S., Tetens F., Kauffold J., Steger K., Fischer B.,
                                                                                                 Capra hirous (Goat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                            "Molecular cloning and localization of caprine relaxin-like factor (RLF) mRNA within the goat testis.", Mol. Reprod. Dev. 53:135-141(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gorilla gorilla (gorilla).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44.7%; Score 67; DB 6; Length 131; 50.0%; Pred. No. 0.013;
                                                                                                                                                                                                                                                                                                                    Hombach Klonisch S., Klonisch T.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-: SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
-: SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
-: SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
EMBL; AF233686; AAF60301.1; -
InterPro: FR000739; Insulin_IGF_relaxin.
Flam; PF00049; Insulin: 1.
SWART; SM00078; IIGF; I.
FROSITE; PS00262; INSULIN; 1.
SEQUENCE 131 AA; 14160 MW; 2A82EB59EA07313A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Indels
                                                              01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33 AA; 3710 MW; 8AC798A03481D2EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Frain-RG YK 287;
Evans B.B.A., Fu P., Tregear G.G.W.;
Evans B.B.A., Fu P., Tregear G.G.W.;
Characterisation of primate relaxin genes.";
J. Mol. Endocrinol. 0:0-0(1993).
EMBL; 227227; CAA81741.1;
HSSP; P04090; GRLX.
                             131 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                               01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 RLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32 KLCGHHSVRALVRLCGGPRW 51
                                                                                                                                        Bovidae; Caprinae; Capra.
NCBI_TaxID=9925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10; Conservative
                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RELAXIN (FRAGMENT).
                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                          TISSUE-TESTIS;
                                                                                                                                                                                              TISSUE-TESTIS:
                                                                                                                                                                                                                                   Klonisch T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                       09N0Z8
                         09N0Z8
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        028429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    028429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
RESULT
             G9N0ZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            028429
                         δ
```

```
ö
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=99115216; PubMed=9915995;
Klonisch T., Hombach-Klonisch S., Froehlich C., Kauffold J.,
Steger K., Huppertz B., Fischer B.;
"Nucleic acid sequence of feline preprorelaxin and its localization
within the feline placenta ";
Biol. Reprod. 60:305-311(1999).
                                                                                                                                                                                                                                                                                                                                             Eŭkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Perissodactyla, Equidae, Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               dasegawa T.;
"Nucleotide sequence of equine Leydig cell-specific insulin-like
                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
   42.0%; Score 63; DB 6; Length 33; 52.4%; Pred. No. 0.012; 7; Indels Live 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Hombach-Klonisch T.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
BRLSP; PA733688; AAF60303.1; -.
HSSP; PA704099; FRIX.
InterPro; IPR000739; Insulin_IGF_relaxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 61; DB 6; Length 73;
Pred. No. 0.056;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB033169; BAA97580.1;
NON_TER 1 1 1
NON_TER 73 73
                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
LEYDIG CELL-SPECIFIC INSULIN-LIKE PEPTIDE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                       73 AA.
                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-THOROUGHBRED; TISSUE=TESTIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                        7 VRLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.7%;
                                                                                            8 IKLCGCELVRAQIAICGMSTW
Query Match
Best Local Similarity 52.4%
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 52.97
Fig. 2.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 GREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | |:||:: ||| ||
| GHHFVRALVRVCGGPRW 17
                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                Equus caballus (Horse).
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hasegawa T
                                                                                                                                                                                                   Q9N0F2
Q9N0F2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09MYK8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9MYK8
                                                                                                                                                                 œ
```

```
SMART; SMO078; I1GF; 1.
PROSITE; PS00262; INSULIN; 1.
SEQUENCE 199 AA; 22386 MW; F69BBD7E4F4A8089 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity.
                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-DO PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                               SECUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                028782
                                                                                                                                                                                                                      Q9TRG5;
                                                                                                                                                                                                         Q9TRG5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
                                                                                                                                                                                RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                              Q9TRG5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δò
                                                                                                                     ô
                                                                                                                                                                                                                                  SOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                            ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Camelus dromedarius (Dromedary) (Arabian camel).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Cameluse; Camelus
                                                                                                                                                                                                                                                                                                Papio hamadryas (Hamadryas baboon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                 Evans B.B.A., Fu P., Tregear G.G.W.;
"Characterization of two relaxin genes in the chimpanzee.";
". Mol. Endocrinol. 140:385-392(1994).
EMBL; 227224; CA81738.1; -.
HSSP; P04090; GRLX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-20191540; PubMed-10727251;
Hombach-Klonisch S., Abd-Elnaeim M., Skidmore J.A., Leiser
Fischer B., Klonisch T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Ruminant relaxin in the pregnant one-humped camel.";
Bloi. Reprod. 62:189-846(2000).
-!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
BRISP: P01348; ARF67741.1;
-- HSSP: P01448; IRLX.
InterPro; IPRO00739; Insulin_IGF_relaxin.
                                                                  Score 61; DB 6; Length 180;
Pred. No. 0.14;
3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 38.0%; Score 57; DB 6; Length 33; Best Local Similarity 52.6%; Pred. No. 0.1; Matches 10; Conservative 3; Mismatches 6; Indels
                  PROSITE; PS00262; INSULIN; 1.
SEQUENCE 180 AA; 20360 MW; 4C2CF371C698AF9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 33 AA; 3618 MW; DD8498A0353F9281 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         199 AA.
                                                                                                                                                                                                             33 AA.
                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                             PRT;
                                                                                                                                     30 LKACGREFVRLQIRICGSLSW 50
                                                                                                                       7 VRLCGREFIRAVIFTCGGSRW 27
                                                                    Query Match 40.7%;
Best Local Similarity 47.6%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 VRLCGREFIRAVIFTCGGS 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                             PRELIMINARY;
          SMART; SM00078; ILGF; 1.
                                                                                                                                                                                                                                                                                                                                       Cercopithecinae; Papio.
                                                                                                                                                                                                                                                                         RELAXIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9838;
                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PREPRORELAXIN
                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-BABA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       910N60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9N0T9
                                                                                                                                                                                                             028788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
                                                                                                                                                                                      RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                610N6C
                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DR
DR
SQ
                                                                                                                                                g
```

```
ö
                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDILINE-93257096; PubMed-8489740;
Kohsaka T., Takahara H., Sugawara K., Tagami S.;
"Endogenous heterogeneity of relaxin and sequence of the major form in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pongo pygmaeus (Orangutan).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metažoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
0
                                               ;
0
Query Match
38.0%; Score 57; DB 6; Length 199;
Best Local Similarity 47.6%; Pred. No. 0.65;
Matches 10; Conservative 2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 6; Length 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           225468D127FE9292 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Piol. Chem. Hoppe-Seyler 374:203-210(1993).
HSSP; P01348; 1RLX.
SEQUENCE 29 AA; 3293 MW; 661A9F5DDDE5DB10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Last Sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
RELAXIN R-III B CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 6;
0.29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Evans B.B.A., Fu P., Tregear G.G.W.;
"Characterisation of primate relaxin genes.";
J. Mol. Endocrinol. 0:00(1993).
HSSP; P04090; GRLX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.7%; Score 55; DB 6
38.1%; Pred. No. 0.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 AA.
                                                                                                                                                                                                                                                       29 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 0.18
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 54;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 VRLCGREFIRAVIFTCGGSRW 27
                                                                                                                                            32 VKACGRELVRLWIEICGSVSW 52
                                                                                               7 VRLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 33 AA; 3752 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pregnant sow ovaries."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RELAXIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                            Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9600;
```

```
Search completed: June 27, 2002, 16:16:29 Job time: 498 sec
                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>;</u>;
            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chung-Sun A., Ji-Tae K., Won-Jin K., Won-Young Y., "Nif-gene organization and nucleotide sequences from Frankia EuIK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mitochondrion.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthomorpha; Acanthopterygii; Stephanoberyciformes; Cetomimidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-21519020; PubMed-11606696;
MAIVA M., Kawaguchi A., Nishida M.;
Mitogenomic exploration of higher teleostean phylogenies: A case study for moderate-scale evolutionary genomics with 38 newly determined complete mitochondrial DNA sequences.";
Mol. Biol. Evol. 18:1993-2009(2001).
         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 494;
         6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Frankia sp. (strain EuiKl).
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Frankineae; Frankiaceae; Frankia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF119361; AAD17362.1;
InterPro; IPR000318; Nitrognse_compl.
InterPro; IPR000510; Oxidored_nitrognse_1.
Pfam; PF00148; oxidored_nitro; 2;
PROSITE; PS00099; NITROGENASE_1_1; 1.
PROSITE; PS000909; NITROGENASE_1_2; 1.
SEQUENCE 494 AA; 53478 MW; OC56192C3A567770 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                             01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     094855;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NADH DEHYDROGENASE SUBUNIT 5.
                                                                                                                                                                                                                                                                                PRT; 494 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     612 AA
   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 34.3%; Score 51.5; I Best Local Similarity 50.0%; Pred. No. 12; Matches 12; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    340 PYRERLAGR---RAVLYTGGVKSW 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 PYGVRLCGREFIRAVIFTCGGSRW 27
                                                         7 VRLCGREFIRAVIFTCGGS 25
                                                                                         8 IKVCGRELVRVQIAICGMS 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Danacetichthys galathenus.
9; Conservative
                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=EUIK1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=143336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=47227;
                                                                                                                                                                                                                                                                                                      Q9Z5Y5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    strain.
                                                                                                                                                                                                                                                                      Q925Y5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              094555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Miya M.
                                                                                                                                                                                                             RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
Q94SS5
Matches
                                                                                                                                                                                                                                         Q925Y5
                                                            ŏ
                                                                                                                g
                                                                                                                                                                                                                                                                         ID DAY DAY REP BE REP B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ογ
```

```
Gaps
                                                                                                                              ö
                                                                                   Query Match
34.0%; Score 51; DB 8; Length 612;
Best Local Similarity 42.1%; Pred. No. 17;
Matches 8; Conservative 4; Mismatches 7; Indels
                                   612 AA; 67303 MW; 3D412F049DAF4907 CRC64;
                                                                                                                                                                                333 VHICTHAFFKAMLFLCSGS 351
EMBL; AP002936; BAB70258.1;
                                                                                                                                                          7 VRLCGREFIRAVIFTCGGS 25
                    Mitochondrion.
                                 SEQUENCE
S W S
                                                                                                                                                            δλ
```

ö